

1 2 3 4

[illegible]

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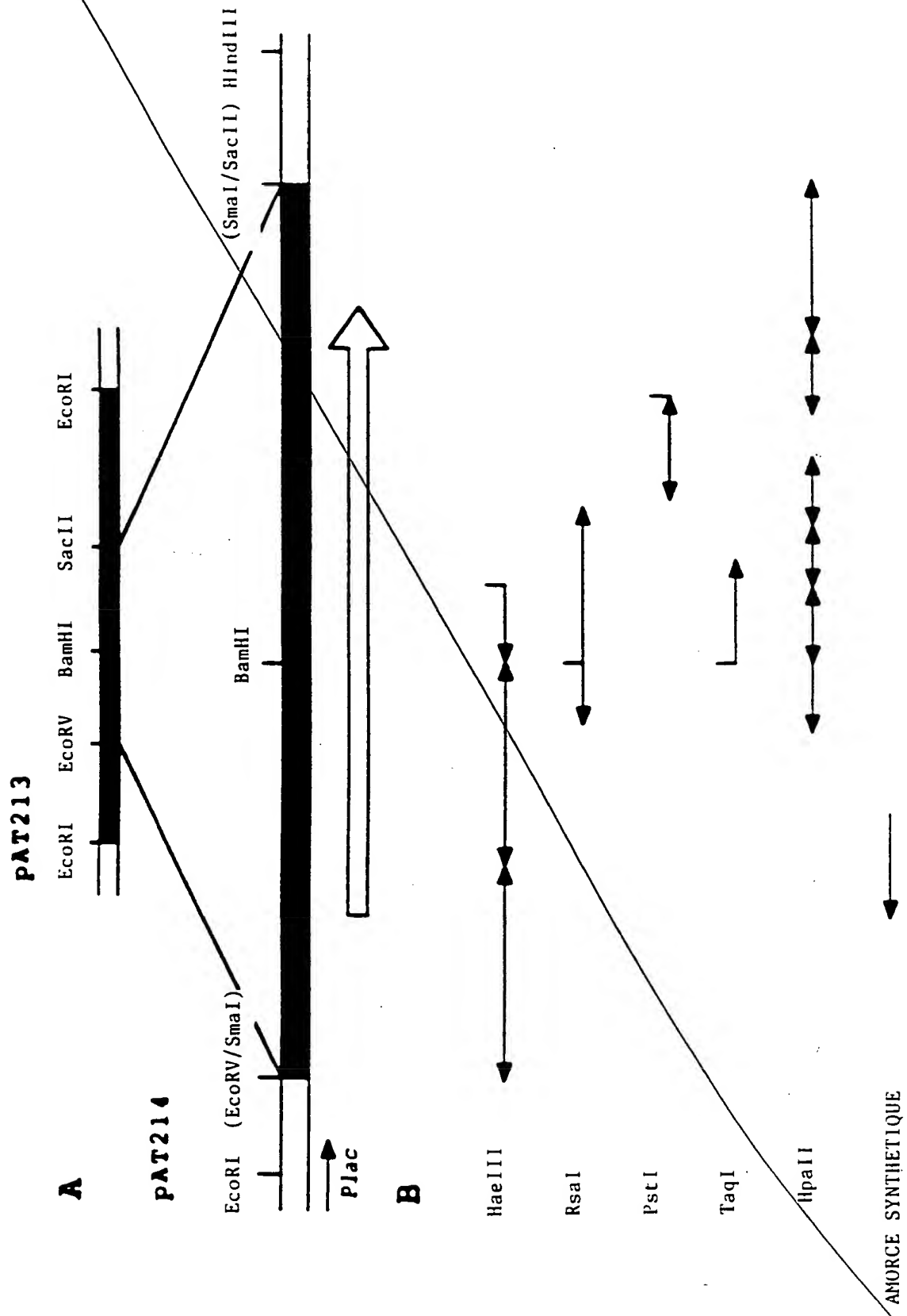


FIGURE 2

FIGURE 3 (T/2)

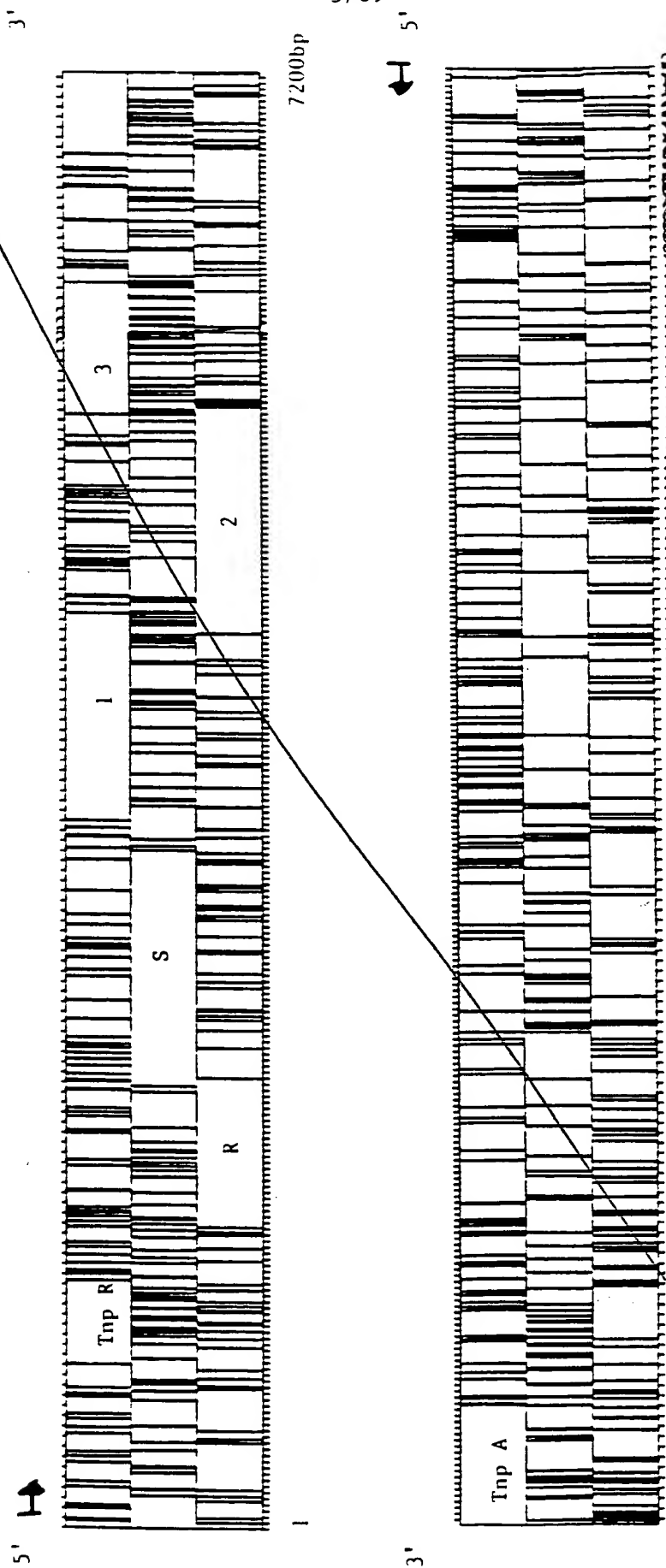
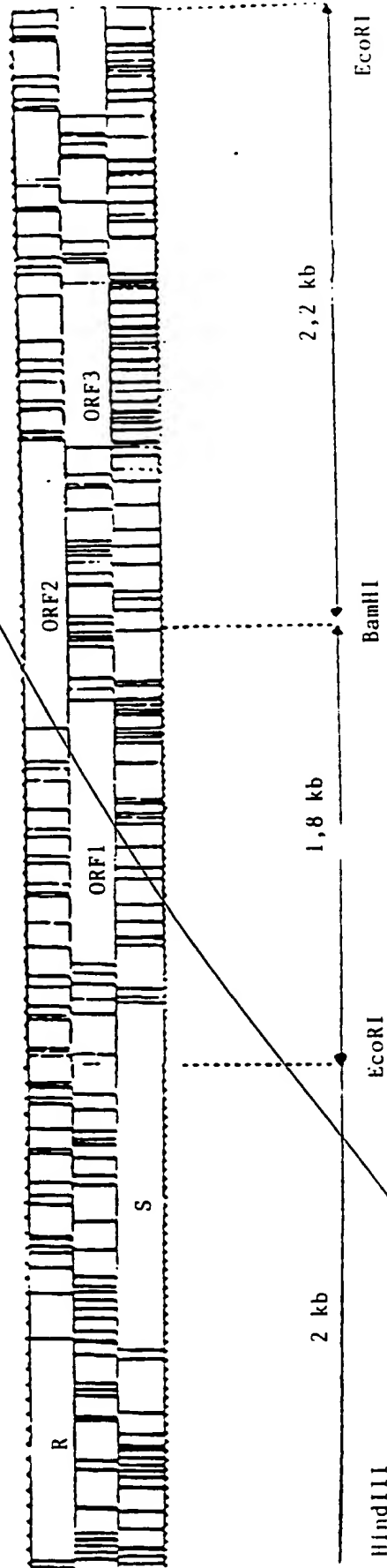


FIGURE 3 (2/2)



AAGCTTTTCTTTTGCTCATTTGTTAGAGATTTACTAACCGTATTAAATAGCTTCTTTTC
AGCCATTGCCCTTGCTTCCACACCATTTCTTCAAGTGTAGTGATAGCAGGCAGTATAAT.
TTTGTTTTTCTTAGAAATCTATGCATTCATGCAGTAGATGAATGGCATCACCATTTTTC
CAAGGCTAATTGATGAAGGTACTTAAATGTTCATTCGATATTCACTCAGGGTAAAGTTAC
AAAGTCGTATTCACCTTCGAATTTCTTCAAAATGATCCCAAAGTGATTTTCCCTTTGAGG
ATAATGATCAAGCGAGGATGGACTAACACCAATCTGTTTCGATATATATGTATGACCCGA
ATCTGGGATGCTTTTGATATGAGTGATGCGCAACCGGATACCGAAGAACAGCTAATTG
AACAGGCAATCCTAAACGGTTTTCTTCCCTCCCTCGCTTATTAACTATTCTAAATCCCG
TTTTGGAAAGAGTGAGTCCCGTAGTTCCATTCATCTTCAGGGATTTGCATAAAAGC
CTGTCCTCTGTTCCGGTGAAGCAATCTCTACCTCTCGCAATTTTCATTTCAGTATCATTC
CATTTCTGTATTTTCATTTATTAGTTCAATTATATATATCAATAGAGTGACTCTATTGAT
ACAAATGTAGTACTGATAAATCATAGTTAAGAGCGTCTCATAGACTTGTCTCAAAH
ATGAGGTGATATTTGCGGAAATCGGTATATTCGTGTCAGTTCGACTAACCGAATCC
TTTCAAGACAAATTCAGCAETTGACCGAGATCGGAATGGATATATATAAGAGAAAGTTT
CAGGAGCAACAAGGATCGGAGCAACTTCAAAAGTGTTAGACGATTTACAGGAAGATG
ACATCATTTATGTTACAGACTTAACTCGAATCACTCGTAGTACACAAGATCTATTGAT
TTAATCGATAACATACGAGATAAAGGCAAGTTTAAATCACTAAAGATACATGGCTTG
ATTTATCAGGAGATAATCCATACAGCCAAATCTTAATTACTGTAAITGGCTGTTAACCC
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AAGGAAAGTTTAAAGGTCGATTAAAGANGTATCATAAAAATCACGCAGGGAATGAATTATG
CGGXAAAGCTATATAAGAGAGGAAATATGACTGTAAATCAAAATTCGTAAGAAATTACTAAT
GTATCTAGGGCTTCATTTATACAGGGAATTTATCAGAAGTGAATAATTAGCCATCTGTATT
CCGCTAATGGGCAATATTTTAAAGAGAAAGGAACCTATAAAATATTAAACAGCCTCCT
AGCGATGCGGAAAGCCCTTTTGATAAAGAAAGGATCATCATCTTAAGAAATCTTAGTCA
TTTATTATGTAAATGCTTATAAATTCGGCCCTATATGCTGATAAATATTAAAGGCAAC

66020" 522560

TTATGTGAAAGGGTGATAACTATGAGCGGATAAATACTTATTGTGGATGATGAACATGAA
ATTGCCGATTGGTTGAATTATACCTTAAACACGAGATTTATACGGTTTTCAAATACATAT
ACCGCCAAAGAGCATTTGGAAATGTATAGACAAAGCTTGAGATTGACCTTGCCATATGGAC
ATCATGCTTCCGGCACAGCGGCTTACTATCTGTCAAAATAAGGGGACAGCACACC
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ATCGGCGGGGATGATTATATAACGAAGCCCTTCGCCACCTGGAGTTAATTGCTCGGGTA
AAGGCCAGTTGCGCGGATACAAAATTCAGTGGAGTAAGGAGCAGAACGAATAATGTT
ATCGTCCACTCCGGCTTGTCATTAAATGTTAACACCCCATGAGTGTATCTGAACGAGAAG
CAGTTATCCCTTACTCCACCGAGTTTCAATACCTGCGAATCCCTCTGTGAACACAGGGG
AATGTGGTTAGCTCCGAGCTGCTATTTCATGAGATATGGGGCGACGAATATTTTCAGCAAG
AGCAACAACACCATCACCGTGCATATCCGGCAATTCGCGAATAAATGAACGACACCAT
GATAATCCGAATATATAAAACCGGATATGGGGGTTGGTTATAAATTGAAATAAATAA
AAACGACTATTCGAGTTGTATATTCGTTCAATGATCCGAGGGAACCTTGGGGATTGGAT
AGCAATTGTATTTCGAGTGTATATGACTTAAATCACCTGGACCGGATGAATATATCA
CTTAAGTATTTTGGAAACAAATATAGATATCTTTATTTATGTGGCGATTGTCATTAGTATCT
TATTCTATGTGCGGTCATGCTTTCAAAATTCGCAAAATGACGAGATTAATACCGG
CATTGATGTACTTATTCAGAACGAGATAACAAATTGAGCTTCTCGGGAATGGATGT
TATGGAAACAAGCTCAACACATTAACACGACCTCGGAAAGCGAGAGCAGGATGCAAA
GCTGGCCGACAAAGAAATGACGTGTTATGTACTTGGCGCACGATATTAAACGCC
CCTTAAATCCATTATCGGTTATTTGAGCTGCTTGACGAGGCTCCAGACATGCCGCTAGA
TCAAAAGGCAAGTATGTGCATATCACGTTGGACAAAGCGTATCGACTCGAACAGCTAAT
CGACGAGTTTGTGAGATTACACGGTATAACCTACAAACGATACGCTAACAAAAACGCA
CATAGACCTTACTATATGCTGCTGAGATGACCGATGAATTTATCTCAGCTTTCGGC
ACATGGAAACACAGCGGTTATTACGCGCCCGAGGATCTGACCGTGTCCGGCGACCTGA

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66020 32560

TAACTCGGAGAGTCTTAAACAACATTTGAAAAACGCCGCTGCATACAGTGAGGATAA
 CAGCATCATTGACATTACCGGGGCTCTCCGGGGATGTGGTGTCAATCGAATTCAGGAA
 CACTGGAGCATCCCAAAGATAAGCTAGCTGCCATATTGAAAGATTCTATAGGCTGGA
 CAATTCTCGTTCTCCGATACGGGTGGCGGGACTTGGATTGGCGATTGCAAGGAAAT
 TATTGTTTCAAGCATGGAGGCGAGATTACGCGGAAGCTATGATAACTATACGACGTTTAG
 GGTAAGGCTTCCAGCGATGCCAGACTTGGTTGATAAAGGAGGTCCTAAGAGATGTATAT
 AATTTTTAGGAAATCTCAAGGTATCTTTACTTTTCTTAGGAAATTAACAATTTAAT
 ATTAAGAAACGGCTCGTTCTTACAGGTAGACTTAATACCGTAAGAACGAGCCGTTTTCG
 TTCTTCAGAGAAAGATTTGACAAGATTACCATTGGCAAGCCGCTTTATTTGGTGCCCTT
 CACAGAAAGGGTTGGTCTTAATATGAATAACATCGGCATTACTGTTTATGGATGTGAGC
 AGGATGAGGCGAGATGCATTCCATGCTCTTCGCTCGCTTTGGCGTTATGGCAACGATAA
 TTAACGCCAACGTGTCGGAATCCAACGCCAATCCGCGCTTCAATCAATGATCAGTG
 TGGGACATAAATCAGAGATTTCGCGCTCTATTCTTCTTGGCGTGAAGAGAGCCGGTGTGA
 AATATATTCTACCCGAAGCATCGGCTGCAATCATATAGATACAACTGCTGCTAAGAGAA
 TGGGCATCACTGTCGACAAATGTGGCTACTCGCCGGATAGCGTTGCCGCTGTGGAAACATG
 TGCTAATTCTTATGGCAGTACGCAAGGTACTCAGCGACATGACAGTTGGTGTGGTGG
 ATTTTCAGGTGGACAGCGACCGTGGCAAGGTATATGAGCGGCTGCGAGGATTGGATGTAAAGTGT
 GAACGGGCCAGATAGGCAAGCGGTATGAGCGGCTGCGAGGATTGGATGTAAAGTGT
 TGGCTTATAGTGGAGCCGAGTATAGAGGTAACTATGTACCGTTTGGATGAGTTGCTGC
 AAAATAGCGATATCGTTACGCTTCAATGTGCGGCTCAATACGGATACGCACTATATTATCA
 GCCACGAAGAAATACAGAGAAATGAGCAAGGAGCATTTCTTATCAATACGCGCGGCTC
 CACTTGTAGATACCTATGAGTTGGTTAAGCATTAGAAACGGGAACCTGGCGGGTGCCG
 CATTGGATGTATTGGAAGGAGGAGAGGTTTCTACTCTGATTGCACCCCAAAACCAA
 TTATATAATCAATTTTACTTAACCTTCAAGAGATGCTTACGTTGATAATCACACCGCAT
 GGGCTATTATACGAGCAAGCGTTGCGTGATACCGTTGAAAAACCATTAAGAACTGTT

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TGGATTTTGAAAGGAGACAGGAGCATGAATAGAAATAAAGTTGCAATACTGTTTGGGCGT
TGCTCAGAGGAGCATGACGTATCGGTAAATCTGCAATAGAGATAGCCGCTAACATTAAT
-AAGBAAAATAGGAGCGTTATACATTGGAATTACGAATCTGGTGTATGGAAATGTGC
GAAAAACCTTGCGCGGATGGGAAACGACAATTGCTATTGAGCTGTACTCGCCGGAT
AAAAAATGACCGGATTACTTGTTAAAGAACCATGAAATAGAAATCAACCATGTGTGAT
GTAGCATTTTCAGCTTTGCAATGGCAAGTCAGGTGAGATGGAATCAATCAAGGTCGT
GAATGTCCGGTATCCCTTTTGTAGGCTGCGATATCAAGGCTCAGCAATTGTATGGAC
AAATCGTTGACATACATCGTTGCGAAATGCTGGGATAGCTACTCCGCTTTTGGGTT
ATTATAAGATGATAGGCCGTTGCGAGCTACGTTTACCTATCTGTTTGTAGCCG
GCGCTTCAGGCTCATCCTTCGGTGTGAAGAAAGTCAATAGCGGACGAATTGGACTAC
GCAATTGAATCGCAAGACAAATATGACAGCAAAATCTTAATTGAGCAGGCTGTTTCGGC
TGTAGGTCGGTTGTGCGGTATTGGGAACAGTGCCGCTTAGTTGTTGGCAGGTTGGAC
CAAATCAGGCTGCAGTACGGAACTTTTCGTATTCATCAGGAAGTCGAGCCGGAAAGGC
TCTGAACACGCGAGTTATAACCGTTCCCGCAGACCTTTCAGCAGAGGAGCGAGGACGATA
CAGGAAACGGCAAAATAATAAAGCGCTCGGCTGTAGAGGCTAGCCCGTGTGGAT
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ACGTATACAGTCGTATATCCCGTATGATGCGCGCTGCHAGGTATTGCACTTCCCGAAGT
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TCACCGGAAACCGGTTGACCGTTATGAAGTAAATCGCATGTAGGGACATACGAGTTGG
CTGAATCGCTTTGAAGGCAAGAGACTGCTGCTACCCAGGATACGATGCTTCTAT
GGACGGTTACCGTCCTAAGCGTGTGTAACCTGTTTATGCAATGGGCTGCACAGCCGG
AAATAACCTGACAAAGGAAGTTATTATCCCAATATTGACCGAAGTGAATTTCA
AAGGATACGTGGCTTCAAAATCAAGCCATAGCCGCGAGTGCCATTGATCTTACGCTT
ATCGATTAGACACGGGTGAGCTTGTACCAATGGGGAGCCGATTGATTTTATGGATGAC

Fig. 4 (4/5)

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GCTCTCATGCGGCAAAATGGAAATATCATGCAATGAAGCGCAAAATCGCAGACGTTTGC
GCTCCATCATGGAAACAGTGGGTTTGAAGCATATAGCCTCGAATGGTGGGACTATGTAT
TAAGAGACGAACCATACCCCAATAGCTATTTGATTTCCCGTTAAATAAACTTTTAACC
GTTGCACGGACAACATATAGCTAGCTCTTTCCGAGGAAACCGGACGTATGTAACTG
GTTCTTAGGGAATTTATATATAGTAGATAGCTTGAAGATGTAAAGCAGAGCGATATTGC
GGTCATTATCTGCGTGCGCTGCGCAAGATAGCCTGATATAAGACTGATCGCATAGAGG
GGTGGTATTTACACCGGCCATTGTCAACAGGCGTTCAGCCTCGTTAAATTCAGCATGG
GTATCACCTTATGAAAATTCATCTACATTTGGTGATATAAGTAAATCCAGTAGGCGAAATA
ATTGACTGTAAATTTACGGGGCAAAACGGCACATCTCAACGAGATTGTGCCGTTTAAGG
GGAGATTCTAGAAATATTTTCATACCTTCGAACTATATAGTTAAGGAGGAGACTGAAATG
AAGAAGTTGTTTTTTTATTTGTTATTTCTTAAATATACTTAGGTTATGACTACGTT
AATGAAGCACGTGTTTCTCAGGAAAGTTCGAATTTCAAAATTTATGATCAAAATCCCAA
GAACATTTAGAAATAGTGGGACTTCAGAAATACCCAGAGAAACATTTACAGAGAA
CAGGTTTATCAAGGAATCTGCTATTAAATCAATAGTAAATATCTGTTCCCAAGAGTG
TGAAGTCAGATATCGTGAATTTATCTAAACATGACGAAATTAATAATGGATACGGGTTGC
TTGATAGTAATATTTATATGTCAAAAGAAATAGCACAAATTTTCAGAGATGCTCAATG
ATGCTGTAAGGGTGGCTTAGTCAATTTATTTATTTAGTGGCTATCGAGACTTTGATG
AGCAAAGTGCTTTACCAAGAAATGGGGCTGAGTATGCCCTACCAAGGTTATAGTG
AGCATAAATTCAGGTTTATCACTAGATGTAGGATCAAGCTTGACGAATGGAAACGAGGCC
ICTGAAGGAAAGTGGATAGAGAAATGCTTGGAAATACGGGTTTCATTTACGTTATCCAG
AGGACAAACAGAGTTAACAGGAATTC

Fig. 4 (5/5)

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LysLeuPhePheLeuLeuIleCys***ArgPheThrAsnArgIleLys***LeuLeuPhe
 SerPheSerPheCysSerPheValArgAspLeuLeuThrValLeuAsnSerPhePheSer
 AlaPheLeuPheAlaHisLeuLeuGluIleTyr***ProTyr***IleAlaSerPheGln
 AAGCTTTTCTTTTGTCTCATTTGTTAGAGATTTACTAACCGTATTAAATAGCTTCTTTTC

 SerHisCysProCysPheProHisHisSerPheLysCysSerAspSerArgGlnTyrAsn
 AlaIleAlaLeuAlaSerHisThrIleLeuSerSerValValIleAlaGlySerIleIle
 ProLeuProLeuLeuProThrProPhePheGlnVal*****GlnAlaVal***Phe
 AGCCATTGCCCTTGCTTCCCACACCATTCTTTCAAGTGTAGTGATAGCAGGCAGTATAAT
 100
 PheValPheSer***LysIleTyrAlaPheMetGln***MetAsnGlyIleThrIlePhe
 LeuPhePheLeuArgLysSerMetHisSerCysSerArg***MetAlaSerProPheSer
 CysPhePheLeuGluAsnLeuCysIleHisAlaValAspGluTrpHisHisHisPhePro
 TTGTGTTTTTCTTAGAAAATCTATGCATTCATGCAGTAGATGAATGGCATCACCATTTTC

 GlnSer***LeuMetLysValLeuLysCysHisSerIlePheThrGlnGlyLysSerTyr
 LysAlaAsn*****ArgTyrLeuAsnValIleArgTyrSerLeuArgValLysValThr
 LysLeuIleAspGluGlyThr***MetSerPheAspIleHisSerGly***LysLeuGln
 CAAAGCTAATTGATGAAGGTACTTAAATGTCATTCGATATTCACCTCAGGGTAAAGTTAC
 200
 LysValValPheThrSerAsnPhePheGlnMetIleProLysCysIlePheProLeuArg
 LysSerTyrSerLeuArgIleSerPheLys***SerGlnSerValPheSerLeu***Gly
 SerArgIleHisPheGluPheLeuSerAsnAspProLysValTyrPheProPheGluAsp
 AAAGTCGTATTCACCTTCGAATTTCTTTCAAATGATCCCAAAGTGTATTTTCCCTTTGAGG
 300

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IleMetIleLysArgGlyTrpThrAsnThrAsnLeuPheArgTyrIleLeuTyrAspArg
 *****SerSerGluAspGlyLeuThrProIleCysPheAspIleTyrCysMetThrGlu
 AsnAspGlnAlaArgMetAsp***HisGlnSerValSerIleTyrIleVal***ProAsn
 ATAATGATCAAGCGAGGATGGACTAACACCAATCTGTTTCGATATATATTGTATGACCGA

 IleTrpAspAlaPheAspMetSerValTrpProThrGlyIleProLysAsnSer***Leu
 SerGlyMetLeuLeuIle***ValTyrGlyGlnProGlyTyrArgArgThrAlaAsn***
 LeuGlyCysPhe***TyrGluCysMetAlaAsnArgAspThrGluGluGlnLeuIleGlu
 ATCTGGGATGCTTTTGTATATGAGTGTATGGCCAACCGGGATACCGAAGACAGCTAATTG
 400
 AsnSerLysSer***ThrValPhePheProProSerLeuIleAsnTyrPhe***IlePro
 ThrAlaAsnProLysArgPheSerSerLeuLeuArgLeuLeuThrIleSerLysSerArg
 GlnGlnIleLeuAsnGlyPheLeuProSerPheAlaTyr***LeuPheLeuAsnProVal
 AACAGCAAATCCTAAACGGTTTTCTTCCCTCCTTCGCTTATTACTATTTCTAAATCCCG

 PheGlyLysSerGluValGlyProGlnTyrProPheIlePheArgAspLeuHisLysSer
 LeuGluLysValLys***ValProSerIleHisSerSerSerGlyIleCysIleLysAla
 TrpLysLys***SerArgSerProValSerIleHisLeuGlnGlyPheAla***LysPro
 TTTGGAAAAAGTGAAGTAGGTCCCCAGTATCCATTTCATCTTCAGGGATTTCATATAAAGC
 500
 LeuSerLeuPheArgCysLysGlnPheSerThrSerArgAsnPheHisSerValSerPhe
 CysLeuCysSerGlyValSerAsnSerLeuProLeuAlaIlePheIleGlnTyrHisSer
 ValSerValProVal***AlaIleLeuTyrLeuSerGlnPheSerPheSerIleIlePro
 CTGTCTCTGTTCCGGTGTAAGCAATTCTCTACCTCTCGCAATTTTCATTTCAGTATCATTC
 600

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HisPheCysIlePheAsnLeuLeuValGlnLeuTyrIleAsnArgValTyrSerIleAsp
 IleSerValPheSerIleTyr***PheAsnTyrIleSerIleGluCysThrLeuLeuIle
 PheLeuTyrPheGlnPheIleSerSerIleIleTyrGln***SerValLeuTyr***Tyr
 CATTCTGTATTTTCAATTTATTAGTTCAATTATATATCAATAGAGTGTACTCTATTGAT

 ThrAsnValValAsp*****AsnHisSer***GluArgLeuIleArgLeuValSerLys
 GlnMet*****ThrAspLysIleIleValLysSerValSer***AspLeuSerGlnLys
 LysCysSerArgLeuIleLysSer***LeuArgAlaSerHisLysThrCysLeuLysAsn
 ACAAATGTAGTAGACTGATAAAATCATAGTTAAGAGCGTCTCATAAGACTTGTCTCAAAA
 700
 MetArg***TyrPheAlaGluAsnArgLeuTyrSerCysGlnPheAsp***ProGluSer
 ***GlyAspIleLeuArgLysIleGlyTyrIleArgValSerSerThrAsnGlnAsnPro
 GluValIlePheCysGlyLysSerValIlePheValSerValArgLeuThrArgIleLeu
 ATGAGGTGATATTTTGCAGAAAATCGGTTATATTCGTGTCAGTTCGACTAACCAGAATCC

 PheLysThrIleSerAlaValGluArgAspArgAsnGlyTyrTyrIleLysArgLysPhe
 SerArgGlnPheGlnGlnLeuAsnGluIleGlyMetAspIleIle***ArgGluSerPhe
 GlnAspAsnPheSerSer***ThrArgSerGluTrpIleLeuTyrLysGluLysValSer
 TTCAAGACAATTTTCAGCAGTTGAACGAGATCGGAATGGATATTATATAAAGAGAAAGTTT
 800
 GlnGluGlnGlnArgIleAlaSerAsnPheLysLysCys***ThrIleTyrArgLysMet
 ArgSerAsnLysGlySerArgAlaThrSerLysSerValArgArgPheThrGlyArg***
 GlyAlaThrLysAspArgGluGlnLeuGlnLysValLeuAspAspLeuGlnGluAspAsp
 CAGGAGCAACAAAGGATCGCGAGCAACTTCAAAAAGTGTTAGACGATTTACAGGAAGATG
 900

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ThrSerPheMetLeuGlnThr***LeuGluSerLeuValValHisLysIleTyrLeuAsn
 HisHisLeuCysTyrArgLeuAsnSerAsnHisSer***TyrThrArgSerIle***Ile
 IleIleTyrValThrAspLeuThrArgIleThrArgSerThrGlnAspLeuPheGluLeu
 ACATCATTATGTTACAGACTTAACTCGAATCACTCGTAGTACACAAGATCTATTTGAAT

SerIleThrTyrGluIleLysArgGlnValAsnHis***LysIleHisGlyLeu
 AsnArg***HisThrArg***LysGlyLysPheLysIleThrLysArgTyrMetAla***
 IleAspAsnIleArgAspLysLysAlaSerLeuLysSerLeuLysAspThrTrpLeuAsp
 TAATCGATAACATACGAGATAAAAAGGCAAGTTTAAAATCACTAAAAGATACATGGCTTG

1000

IleTyrGlnLysIleIleHisThrAlaAsnSer***LeuLeu***TrpLeuValLeuThr
 PheIleArgArg***SerIleGlnProIleLeuAsnTyrCysAsnGlyTrpCys***Pro
 LeuSerGluAspAsnProTyrSerGlnPheLeuIleThrValMetAlaGlyValAsnGln
 ATTTATCAGAAGATAATCCATACAGCGAATTCTTAATTACTGTAATGGCTGGTGTTAACC

Asn***SerGluIleLeuPheGly***AspAsnValLysGlyLeuAsnTrpLeuArgLys
 IleArgAlaArgSerTyrSerAspGluThrThr***ArgAsp***IleGly***GluArg
 LeuGluArgAspLeuIleArgMetArgGlnArgGluGlyIleGluLeuAlaLysLysGlu
 AATTAGAGCGAGATCTTATTCGGATGAGACAACGTGAAGGGATTGAATTGGCTAAGAAAG

1100

LysGluSerLeuLysValAsp***ArgSerIleIleLysIleThrGlnGlu***IleMet
 ArgLysVal***ArgSerIleLysGluValSer***LysSerArgArgAsnGluLeuCys
 GlyLysPheLysGlyArgLeuLysLysTyrHisLysAsnHisAlaGlyMetAsnTyrAla
 AAGGAAAGTTTAAAGGTCGATTAAAGAAGTATCATATAAAATCACGCAGGAATGAATTATG

1200

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ArgArgLysLeuTyrLysGluGlyAsnMetThrValAsnGlnIleCysGluIleThrAsn
 GlyGluSerTyrIleLysLysGluIle***Leu***IleLysPheValLysLeuLeuMet
 AlaLysAlaIle***ArgArgLysTyrAspCysLysSerAsnLeu***AsnTyr***Cys
 CGGXXAAAGCTATATAAAGAAGGAAATATGACTGTAAATCAATTGTGAAATTACTAAT

ValSerArgAlaSerLeuTyrArgLysLeuSerGluValAsnAsn***ProPheCysIle
 TyrLeuGlyLeuHisTyrThrGlyAsnTyrGlnLys***IleIleSerHisSerValPhe
 Ile***GlyPheIleIleGlnGluIleIleArgSerGlu***LeuAlaIleLeuTyrSer
 GTATCTAGGGCTTCATTATACAGGAAATTATCAGAAGTGAATAATTAGCCATTCTGTATT

1300

ProLeuMetGlyAsnIlePheLysGluGluLysGluThrIleLysTyr***GlnProPro
 Arg***TrpAlaIlePheLeuLysLysLysArgLysLeu***AsnIleAsnSerLeuLeu
 AlaAsnGlyGlnTyrPhe***ArgArgLysGlyAsnTyrLysIleLeuThrAlaSer***
 CCGCTAATGGGCAATATTTTAAAGAAGAAAAGGAACTATAATATTAACAGCCTCCT

SerAspAlaGluLysProPheAspLysLysArgIleIleIleLeuArgAsnSer***Ser
 AlaMetProLysSerProLeuIleLysLysGluSerSerSer***GluIleLeuSerHis
 ArgCysArgLysAlaLeu*****LysLysAsnHisHisLeuLysLysPheLeuValIle
 AGCGATGCCGAAAAGCCCTTTGATAAAAAAGAATCATCATCTTAAGAAATTCTTAGTCA

1400

PheIleMet***MetLeuIleAsnSerAlaLeu***SerAspLysLeuLeuArgAlaAsn
 LeuLeuCysLysCysLeu***IleArgProTyrAsnLeuIleAsnTyr***GlyGlnThr
 TyrTyrValAsnAlaTyrLysPheGlyProIleIle*****IleIleLysGlyLysLeu
 TTTATTATGTAAATGCTTATAAATTCGGCCCTATAATCTGATAAATTATTAAGGGCAAAC

1500

LeuCysGluArgValIleThrMetSerAspLysIleLeuIleValAspAspGluHisGlu
TyrValLysGly*****Leu***AlaIleLysTyrLeuLeuTrpMetMetAsnMetLys
Met***LysGlyAspAsnTyrGluArg***AsnThrTyrCysGly*****Thr***Asn
TTATGTGAAAGGGTGATAACTATGAGCGATAAAATACTTATTGTGGATGATGAACATGAA

IleAlaAspLeuValGluLeuTyrLeuLysAsnGluAsnTyrThrValPheLysTyrTyr
LeuProIleTrpLeuAsnTyrThr***LysThrArgIleIleArgPheSerAsnThrIle
CysArgPheGly***IleIleLeuLysLysArgGluLeuTyrGlyPheGlnIleLeuTyr
ATTGCCGATTGGTTGAATTATACTTAAAAACGAGAATTATACGGTTTTCAAATACTAT

1600

ThrAlaLysGluAlaLeuGluCysIleAspLysSerGluIleAspLeuAlaIleLeuAsp
ProProLysLysHisTrpAsnVal***ThrSerLeuArgLeuThrLeuProTyrTrpThr
ArgGlnArgSerIleGlyMetTyrArgGlnVal***Asp***ProCysHisIleGlyHis
ACCGCCAAAGAAGCATTGGAAATGTATAGACCAAGTCTGAGATTGACCTTGCCATATTGGAC

~~IleMetLeuProGlyThrSerGlyLeuThrIleCysGlnLysIleArgAspLysHisThr
 SerCysPheProAlaGlnAlaAlaLeuLeuSerValLysLys***GlyThrSerThrPro
 HisAlaSerArgHisLysArgProTyrTyrLeuSerLysAsnLysGlyGlnAlaHisLeu
 ATCATGCTTCCCGGCACAAGCGGCCCTTACTATCTGTCAAAAAATAAGGGACAAGCACACC~~

1700

TyrProIleIleMetLeuThrGlyLysAspThrGluValAspLysIleThrGlyLeuThr
IleArgLeuSerCys***ProGlyLysIleGlnArg***IleLysLeuGlnGly***Gln
SerAspTyrHisAlaAspArgGluArgTyrArgGlyArg***AsnTyrArgValAsnAsn
TATCCGATTATCATGCTGACCGGGGAAAGATACAGAGGTAGATAAAATTACAGGGTTAACA

1800

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IleGlyAlaAspAspTyrIleThrLysProPheArgProLeuGluLeuIleAlaArgVal
SerAlaArgMetIleIle***ArgSerProPheAlaHisTrpSer***LeuLeuGly***
ArgArgGly***LeuTyrAsnGluAlaLeuSerProThrGlyValAsnCysSerGlyLys
ATCGGCGCGGATGATTATATAACGAAGCCCTTTCGCCCCACTGAGTTAATTGCTCGGGTA

LysAlaGlnLeuArgArgTyrLysLysPheSerGlyValLysGluGlnAsnGluAsnVal
ArgProSerCysAlaAspThrLysAsnSerValGlu***ArgSerArgThrLysMetLeu
GlyProValAlaProIleGlnLysIleGlnTrpSerLysGlyAlaGluArgLysCysTyr
AAGGCCCGAGTTGCGCCGATACAAAAAATTCAGTGGAGTAAAGGAGCAGAACGAAAATGTT

1900

IleValHisSerGlyLeuValIleAsnValAsnThrHisGluCysTyrLeuAsnGluLys
SerSerThrProAlaLeuSerLeuMetLeuThrProMetSerValIle***ThrArgSer
ArgProLeuArgProCysHis***Cys***HisPro***ValLeuSerGluArgGluAla
ATCGTCCACTCCGGCCTTGTCATTAATGTTAACACCCATGAGTGTATCTGAACGAGAAG

GlnLeuSerLeuThrProThrGluPheSerIleLeuArgIleLeuCysGluAsnLysGly
SerTyrProLeuLeuProProSerPheGlnTyrCysGluSerSerValLysThrArgGly
ValIleProTyrSerHisArgValPheAsnThrAlaAsnProLeu***LysGlnGlyGlu
CAGTTATCCCTTACTCCCACCGAGTTTTCAATACTGCGAATCCTCTGTGAAAACAAGGGG

2000

AsnValValSerSerGluLeuLeuPheHisGluIleTrpGlyAspGluTyrPheSerLys
MetTrpLeuAlaProSerCysTyrPheMetArgTyrGlyAlaThrAsnIleSerAlaArg
CysGly***LeuArgAlaAlaIleSer***AspMetGlyArgArgIlePheGlnGlnGlu
AATGTGGTTAGCTCCGAGCTGCTATTTTCATGAGATATGGGGCGACGAATATTTTCAGCAAG

2100

17/ 69

SerAsnAsnThrIleThrValHisIleArgHisLeuArgGluLysMetAsnAspThrIle
 AlaThrThrProSerProCysIleSerGlyIleCysAlaLysLys***ThrThrProLeu
 GlnGlnHisHisHisArgAlaTyrProAlaPheAlaArgLysAsnGluArgHisHis***
 AGCAACAACACCATCACCGTGCATATCCGGCATTGCGCGAAAAATGAACGACACCATT

 AspAsnProLysTyrIleLysThrValTrpGlyValGlyTyrLysIleGluLys***Lys
 IleIleArgAsnIle***LysArgTyrGlyGlyLeuValIleLysLeuLysAsnLysLys
 SerGluIleTyrLysAsnGlyMetGlyGlyTrpLeuAsn***LysIleLysLys
 GATAATCCGAATATATAAAAACGGTATGGGGGGTTGGTTATAAAATTGAAAAATAAAAA
 2200
 LysArgLeuPheGlnThrArgThrLysThrLeuHisValTyrArgCysAsnCysCysGly
 AsnAspTyrSerLysLeuGluArgLysLeuTyrMetTyrIleValAlaIleValValVal
 ThrThrIleProAsn***AsnGluAsnPheThrCysIleSerLeuGlnLeuLeuTrp***
 AAACGACTATTCCAACTAGAACGAAACTTTACATGTATATCGTTGCAATTGTTGTGGT

 SerAsnCysIleArgValValTyrSerPheAsnAspProArgGluThrTrpGlyLeuAsp
 AlaIleValPheValLeuTyrIleArgSerMetIleArgGlyLysLeuGlyAspTrpIle
 GlnLeuTyrSerCysCysIlePheValGln***SerGluGlyAsnLeuGlyIleGlySer
 AGCAATTGTATTCTGTGTGTATATTCGTTCAATGATCCGAGGGAACTTGGGGATTGGAT
 2300
 LeuLysTyrPheGlyLysGlnIle***LeuLysSerProGlyArgAspGluIleIleSer
 LeuSerIleLeuGluAsnLysTyrAspLeuAsnHisLeuAspAlaMetLysLeuTyrGln
 ValPheTrpLysThrAsnMetThrIleThrTrpThrArg***AsnTyrIleAsn
 CTTAAGTATTTTGGAAACAAATATGACTTAAATCACCTGGACGCGATGAAATTATATCA
 2400

Fig. 5 (8/25)

000000-000000

IlePheHisThrGluGlnTyrArgTyrLeuTyrLeuCysGlyAspCysHis***TyrSer
TyrSerIleArgAsnAsnIleAspIlePheIleTyrValAlaIleValIleSerIleLeu
IleProTyrGlyThrIle***IleSerLeuPheMetTrpArgLeuSerLeuValPheLeu
ATATTCCATACGGAACAATATAGATATCTTTATTTATGTGGCGATTGTCATTAGTATTCT

TyrSerMetSerArgHisAlaPheLysIleArgLysIleLeu***ArgAspLysTyrArg
IleLeuCysArgValMetLeuSerLysPheAlaLysTyrPheAspGluIleAsnThrGly
PheTyrValAlaSerCysPheGlnAsnSerGlnAsnThrLeuThrArg***IleProAla
TATTCTATGTGCGTCATGCTTTCAAATTCGCAAATACTTTGACGAGATAAATACCGG

2500

His***CysThrTyrSerGluArgArg***ThrAsn***AlaPheCysGlyAsnGlyCys
IleAspValLeuIleGlnAsnGluAspLysGlnIleGluLeuSerAlaGluMetAspVal
LeuMetTyrLeuPheArgThrLysIleAsnLysLeuSerPheLeuArgLysTrpMetLeu
CATTGATGTACTTATTCAGAACGAAGATAAACAATTGAGCTTTCTGCGGAAATGGATGT

TyrGlyThrLysAlaGlnHisIleLysThrAspSerGlyLysAlaArgAlaGlyCysLys
MetGluGlnLysLeuAsnThrLeuLysArgThrLeuGluLysArgGluGlnAspAlaLys
TrpAsnLysSerSerThrHis***AsnGlyLeuTrpLysSerGluSerArgMetGlnSer
TATGGAACAAAAGCTCAACACATTAAACGGACTCTGAAAAGCGAGAGCAGGATGCAAA

2600

AlaGlyArgThrLysLysLys***ArgCysTyrValLeuGlyAlaArgTyr***AsnAla
LeuAlaGluGlnArgLysAsnAspValValMetTyrLeuAlaHisAspIleLysThrPro
TrpProAsnLysGluLysMetThrLeuLeuCysThrTrpArgThrIleLeuLysArgPro
GCTGGCCGAACAAAGAAAAAATGACGTTGTTATGTACTTGGCGCACGATATTAAACGCC

2700

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ProTyrIleHisTyrArgLeuPheGluProAla***ArgGlySerArgHisAlaGlyArg
LeuThrSerIleIleGlyTyrLeuSerLeuLeuAspGluAlaProAspMetProValAsp
LeuHisProLeuSerValIle***AlaCysLeuThrArgLeuGlnThrCysArg***Ile
CCTTACATCCATTATCGGTTATTTGAGCCTGCTTGACGAGGCTCCAGACATGCCGGTAGA

SerLysGlyLysValCysAlaTyrHisValGlyGlnSerValSerThrArgThrAlaAsn
GlnLysAlaLysTyrValHisIleThrLeuAspLysAlaTyrArgLeuGluGlnLeuIle
LysArgGlnSerMetCysIleSerArgTrpThrLysArgIleAspSerAsnSer***Ser
TCAAAGGCAAGTATGTGCATATCACGTTGGACAAAGCGTATCGACTCGAACAGCTAAT

2800

ArgArgValPhe***AspTyrThrVal***ProThrAsnAspAsnAlaAsnLysAsnAla
AspGluPhePheGluIleThrArgTyrAsnLeuGlnThrIleThrLeuThrLysThrHis
ThrSerPheLeuArgLeuHisGlyIleThrTyrLysArg***Arg***GlnLysArgThr
CGACGAGTTTTTTGAGATTACACGGTATAACCTACAAACGATAACGCTAACAAAAACGCA

HisArgProIleLeuTyrAlaGlyAlaAspAspArg***IleLeuSerSerAlaPheArg
IleAspLeuTyrTyrMetLeuValGlnMetThrAspGluPheTyrProGlnLeuSerAla
ThrTyrThrIleCysTrpCysArgProMetAsnPheIleLeuSerPheProHis
CATAGACCTATACTATATGCTGGTGCAGATGACCGATGAATTTTATCCTCAGCTTTCCGC

2900

ThrTrpLysThrGlyGlyTyrSerArgProArgGlySerAspArgValArgArgPro***
HisGlyLysGlnAlaValIleHisAlaProGluAspLeuThrValSerGlyAspProAsp
MetGluAsnArgArgLeuPheThrProProArgIle***ProCysProAlaThrLeuIle
ACATGGAAAACAGGCGGTTATTCACGCCCCGAGGATCTGACCGTGTCGGGCGACCCTGA

3000

20/ 69

ThrArgGluSerLeuGlnHisPheGluLysArgArgCysIleGln***Gly***
LysLeuAlaArgValPheAsnAsnIleLeuLysAsnAlaAlaAlaTyrSerGluAspAsn
AsnSerArgGluSerLeuThrThrPhe***LysThrProLeuHisThrValArgIleThr
TAAACTCGCGAGAGTCTTTAACAACATTTTGAAAAACGCCGCTGCATACAGTGAGGATAA
.
GlnHisHis***HisTyrArgGlyProLeuArgGlyCysGlyValAsnArgIleGlnGlu
SerIleIleAspIleThrAlaGlyLeuSerGlyAspValValSerIleGluPheLysAsn
AlaSerLeuThrLeuProArgAlaSerProGlyMetTrpCysGlnSerAsnSerArgThr
CAGCATCATTGACATTACCGCGGGCCTCTCCGGGGATGTGGTSTCAATCGAATTCAAGAA
.
3100
HisTrpLysHisProLysArg***AlaSerCysHisIle***LysValLeu***AlaGly
ThrGlySerIleProLysAspLysLeuAlaAlaIlePheGluLysPheTyrArgLeuAsp
LeuGluAlaSerGlnLysIleSer***LeuProTyrLeuLysSerSerIleGlyTrpThr
CACTGGAAGCATCCCAAAGATAAGCTAGCTGCCATATTTGAAAGTTCTATAGGCTGGA
.
GlnPheSerPhePheArgTyrGlyTrpArgGlyThrTrpIleGlyAspCysLysArgAsn
AsnSerArgSerSerAspThrGlyGlyAlaGlyLeuGlyLeuAlaIleAlaLysGluIle
IleLeuValLeuProIleArgValAlaArgAspLeuAspTrpArgLeuGlnLysLysLeu
CAATTCTCGTTCTTCCGATACGGGTGGCGCGGGACTTGGATTGGCGATTGCAAAAGAAAT
.
3200
TyrCysSerAlaTrpArgAlaAspLeuArgGlyLysLeu*****LeuTyrAspVal***
IleValGlnHisGlyGlyGlnIleTyrAlaGluSerTyrAspAsnTyrThrThrPheArg
LeuPheSerMetGluGlyArgPheThrArgLysAlaMetIleThrIleArgArgLeuGly
TATTGTTTCAGCATGGAGGGCAGATTTACGCGGAAAGCTATGATAACTATACGACGTTTAG
.
3300

21/69

GlyArgAlaSerSerAspAlaArgLeuGly*****LysGluValLeuArgAspValTyr
 ValGluLeuProAlaMetProAspLeuValAspLysArgArgSer***GluMetTyrIle
 SerPheGlnArgCysGlnThrTrpLeuIleLysGlyGlyProLysArgCysIle
 GGTAGAGCTTCCAGCGATGCCAGACTTG GTTGATAAAAGGAGGTCCTAAGAGATGTATAT

 AsnPheLeuGlyLysSerGlnGlyTyrLeuTyrPhePheLeuGlyAsn***GlnPheAsn
 IlePhe***GluAsnLeuLysValIlePheThrPheSer***GluIleAsnAsnLeuIle
 PhePheArgLysIleSerArgLeuSerLeuLeuPheLeuArgLysLeuThrIle***Tyr
 AATTTTTTTAGGAAAATCTCAAGGTTATCTTTACTTTTTCTTAGGAAATTAACAATTTAAT
 3400
 IleLysLysArgLeuValLeuThrArg***Thr***TyrArgLysAsnGluProPheSer
 LeuArgAsnGlySerPheLeuHisGlyArgLeuAsnThrValArgThrSerArgPheArg
 GluThrAlaArgSerTyrThrValAspLeuIleProGluArgAlaValPheVal
 ATTAAGAAACGGCTCGTTCCTTACACGGTAGACTTAATACCGTAAGAACGAGCCGTTTTTCG

 PhePheArgGluArgPheAspLysIleThrIleGlyIleProValLeuPheGlyAlaPhe
 SerSerGluLysAspLeuThrArgLeuProLeuAlaSerProPheTyrLeuValProPhe
 LeuGlnArgLysIle***GlnAspTyrHisTrpHisProArgPheIleTrpCysLeuSer
 TTCTTCAGAGAAAGATTGACAAGATTACCATGGCATCCCGTTTTATTGGTGCCCTT
 3500
 HisArgLysGlyTrpSer***Leu***IleThrSerAlaLeuLeuPheMetAspValSer
 ThrGluArgValGlyLeuAsnTyrGlu***HisArgHisTyrCysLeuTrpMet***Ala
 GlnLysGlyLeuValLeuIleMetAsnAsnIleGlyIleThrValTyrGlyCysGluGln
 CACAGAAAGGGTTGGTCTTAATTATGAATAACATCGGCATTACTGTTTATGGATGTGAGC
 3600

Fig. 5 (12/25)

22/69

ArgMetArgGlnMetHisSerMetLeuPheArgLeuAlaLeuAlaLeuTrpGlnArg***
 Gly***GlyArgCysIleProCysSerPheAlaSerLeuTrpArgTyrGlyAsnAspAsn
 AspGluAlaAspAlaPheHisAlaLeuSerProArgPheGlyValMetAlaThrIleIle
 AGGATGAGGCAGATGCATTCCATGCTCTTTTCGCCTCGCTTTGCGTTATGGCAACGATAA

LeuThrProThrCysArgAsnProThrProAsnProArgLeuSerIleAsnValSerVal
 ***ArgGlnArgValGlyIleGlnArgGlnIleArgAlaPheGlnSerMetTyrGlnCys
 AsnAlaAsnValSerGluSerAsnAlaLysSerAlaProPheAsnGlnCysIleSerVal
 TTAACGCCAACGTGTCGGAATCCAACGCCAAATCCGCGCCTTCAATCAATGTATCAGTG

3700

TrpAspIleAsnGlnArgPheProProLeuPhePheLeuArg***ArgGluProVal***
 GlyThr***IleArgAspPheArgLeuTyrSerSerCysAlaGluGluSerArgCysGlu
 GlyHisLysSerGluIleSerAlaSerIleLeuLeuAlaLeuLysArgAlaGlyValLys
 TGGGACATAAATCAGAGATTTCGCGCTCTATTCTTCTTGCGCTGAAGAGAGCCGGTGTGA

AsnIlePheLeuProGluAlaSerAlaAlaIleIle***IleGlnLeuLeuLeuArgGlu
 IleTyrPheTyrProLysHisArgLeuGlnSerTyrArgTyrAsnCysCys***GluAsn
 TyrIleSerThrArgSerIleGlyCysAsnHisIleAspThrThrAlaAlaLysArgMet
 AATATATTTCTACCCGAAGCATCGGCTGCAATCATATAGATACAACTGCTGCTAAGAGAA

3800

TrpAlaSerLeuSerThrMetTrpArgThrArgArgIleAlaLeuProIleIleLeu***
 GlyHisHisCysArgGlnCysGlyValLeuAlaGly***ArgCysArgLeuTyrTyrAsp
 GlyIleThrValAspAsnValAlaTyrSerProAspSerValAlaAspTyrThrMetMet
 TGGGCATCACTGTCGACAATGTGGCGTACTCGCCGGATAGCGTTGCCGATTATACTATGA

3900

Fig. 5 (13/25)

DATE	NAME	AGE	SEX	RELATION	RESIDENCE	EDUCATION	RELIGION	STATUS	REMARKS
1945	JOHN	18	M	SON	1234 ST	HIGH SCHOOL	PROTESTANT	WORKING	GOOD
1946	MARY	16	F	DAUGHTER	1234 ST	HIGH SCHOOL	CATHOLIC	WORKING	GOOD
1947	JOHN	15	M	SON	1234 ST	HIGH SCHOOL	PROTESTANT	WORKING	GOOD
1948	MARY	14	F	DAUGHTER	1234 ST	HIGH SCHOOL	CATHOLIC	WORKING	GOOD
1949	JOHN	13	M	SON	1234 ST	HIGH SCHOOL	PROTESTANT	WORKING	GOOD
1950	MARY	12	F	DAUGHTER	1234 ST	HIGH SCHOOL	CATHOLIC	WORKING	GOOD
1951	JOHN	11	M	SON	1234 ST	HIGH SCHOOL	PROTESTANT	WORKING	GOOD
1952	MARY	10	F	DAUGHTER	1234 ST	HIGH SCHOOL	CATHOLIC	WORKING	GOOD
1953	JOHN	9	M	SON	1234 ST	HIGH SCHOOL	PROTESTANT	WORKING	GOOD
1954	MARY	8	F	DAUGHTER	1234 ST	HIGH SCHOOL	CATHOLIC	WORKING	GOOD
1955	JOHN	7	M	SON	1234 ST	HIGH SCHOOL	PROTESTANT	WORKING	GOOD
1956	MARY	6	F	DAUGHTER	1234 ST	HIGH SCHOOL	CATHOLIC	WORKING	GOOD
1957	JOHN	5	M	SON	1234 ST	HIGH SCHOOL	PROTESTANT	WORKING	GOOD
1958	MARY	4	F	DAUGHTER	1234 ST	HIGH SCHOOL	CATHOLIC	WORKING	GOOD
1959	JOHN	3	M	SON	1234 ST	HIGH SCHOOL	PROTESTANT	WORKING	GOOD
1960	MARY	2	F	DAUGHTER	1234 ST	HIGH SCHOOL	CATHOLIC	WORKING	GOOD

Fig. 5 (14/25)

24/69

AlaThrAsnLysTyrArgGlu***SerLysGluHisPheLeuSerIleLeuGlyAlaVal
ProArgThrAsnThrGluAsnGluAlaArgSerIleSerTyrGlnTyrTrpAlaArgSer
HisGluGlnIleGlnArgMetLysGlnGlyAlaPheLeuIleAsnThrGlyArgGlyPro
GCCAGGAACAAATACAGAGAATGAAGCAAGGAGCATTCTTATCAATACTGGGCGCGGTC

HisLeu***IleProMetSerTrpLeuLysHis***LysThrGlyAsnTrpAlaValPro
ThrCysArgTyrLeu***ValGly***SerIleArgLysArgGluThrGlyArgCysArg
LeuValAspThrTyrGluLeuValLysAlaLeuGluAsnGlyLysLeuGlyGlyAlaAla
CACTTG TAGATACCTATGAGTTGGTTAAAGCATTAGAAAACGGGAAACTGGGCGGTGCCG

4300

HisTrpMetTyrTrpLysGluArgLysSerPheSerThrLeuIleAlaProLysAsnGln
IleGlyCysIleGlyArgArgGlyArgValPheLeuLeu***LeuHisProLysThrAsn
LeuAspValLeuGluGlyGluGluGluPhePheTyrSerAspCysThrGlnLysProIle
CATTGGATGTATTGGAAGGAGAGGAAGAGTTTTTCTACTCTGATTGCACCCAAAAACCAA

LeuIleIleAsnPheTyrLeuAsnPheLysGluCysLeuThr*****SerHisArgIle
*****SerIlePheThr***ThrSerLysAsnAla***ArgAspAsnHisThrAlaTyr
AspAsnGlnPheLeuLeuLysLeuGlnArgMetProAsnValIleIleThrProHisThr
TTGATAATCAATTTTTACTTAACTTCAAAGAATGCCTAACGTGATAATCACACCGCATA

4400

ArgProIleIleProSerLysArgCysValIleProLeuLysLysProLeuLysThrVal
GlyLeuLeuTyrArgAlaSerValAla***TyrArg***LysAsnHis***LysLeuPhe
AlaTyrTyrThrGluGlnAlaLeuArgAspThrValGluLysThrIleLysAsnCysLeu
CGGCCTATTATACCGAGCAAGCGTTGCGTGATACCGTTGAAAACCATTAAAACTGTT

4500

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TrpIleLeuLysGlyAspArgSerMetAsnArgIleLysValAlaIleLeuPheGlyGly
 GlyPhe***LysGluThrGlyAla***IleGlu***LysLeuGlnTyrCysLeuGlyVal
 AspPheGluArgArgGlnGluHisGlu***AsnLysSerCysAsnThrValTrpGlyLeu
 TGGATTTTGAAGGAGACAGGAGCATGAATAGAATAAAAGTTGCAATACTGTTTGGGGGT

CysSerGluGluHisAspValSerValLysSerAlaIleGluIleAlaAlaAsnIleAsn
 AlaGlnArgSerMetThrTyrArg***AsnLeuGln***Arg***ProLeuThrLeuIle
 LeuArgGlyAla***ArgIleGlyLysIleCysAsnArgAspSerArg***His*****
 TGCTCAGAGGAGCATGACGTATCGGTAAAATCTGCAATAGAGATAGCCGCTAACATTAAT

4600

LysGluLysTyrGluProLeuTyrIleGlyIleThrLysSerGlyValTrpLysMetCys
 LysLysAsnThrSerArgTyrThrLeuGluLeuArgAsnLeuValTyrGlyLysCysAla
 ArgLysIleArgAlaValIleHisTrpAsnTyrGluIleTrpCysMetGluAsnValArg
 AAAGAAAAATACGAGCCGTTATACATTGGAATTACGAAATCTGGTGTATGGAAAATGTGC

GluLysProCysAlaGluTrpGluAsnAspAsnCysTyrSerAlaValLeuSerProAsp
 LysAsnLeuAlaArgAsnGlyLysThrThrIleAlaIleGlnLeuTyrSerArgArgIle
 LysThrLeuArgGlyMetGlyLysArgGlnLeuLeuPheSerCysThrLeuAlaGly***
 GAAAAACCTTGCGCGGAATGGGAAAACGACAATTGCTATTCAGCTGTACTCTCGCCGGAT

4700

LysLysMetHisGlyLeuLeuValLysLysAsnHisGluTyrGluIleAsnHisValAsp
 LysLysCysThrAspTyrLeuLeuLysArgThrMetAsnMetLysSerThrMetLeuMet
 LysAsnAlaArgIleThrCys***LysGluPro***Ile***AsnGlnProCys***Cys
 AAAAAAATGCACGGATTACTTGTTAAAAAGAACCATGAATATGAAATCAACCATGTTGAT

4800

ValAlaPheSerAlaLeuHisGlyLysSerGlyGluAspGlySerIleGlnGlyLeuPhe
 ***HisPheGlnLeuCysMetAlaSerGlnValLysMetAspProTyrLysValCysLeu
 SerIlePheSerPheAlaTrpGlnValArg***ArgTrpIleHisThrArgSerVal***
 GTAGCATTTCAGCTTTGCATGGCAAGTCAGGTGAAGATGGATCCATACAAGGTCTGTTT

~~GluLeuSerGlyIleProPheValGlyCysAspIleGlnSerSerAlaIleCysMetAsp
AsnCysProValSerLeuLeu***AlaAlaIlePheLysAlaGlnGlnPheValTrpThr
IleValArgTyrProPheCysArgLeuArgTyrSerLysLeuSerAsnLeuTyrGlyGln
GAATTGTCGGGTATCCCTTTTGTAGGCTGCGATATTCAAAGCTCAGCAATTTGTATGGAC~~

4900

~~LysSerLeuThrTyrIleValAlaLysAsnAlaGlyIleAlaThrProAlaPheTrpVal
 AsnArg***HisThrSerLeuArgLysMetLeuGly***LeuLeuProProPheGlyLeu
 IleValAspIleHisArgCysGluLysCysTrpAspSerTyrSerArgLeuLeuGlyTyr
 AAATCGTTGACATACATCGTTGGGAAAAATGCTGGGATAGCTACTCCCGCCTTTTGGGTT~~

~~IleAsnLysAspAspArgProValAlaAlaThrPheThrTyrProValPheValLysPro
LeuIleLysMetIleGlyArgTrpGlnLeuArgLeuProIleLeuPheLeuLeuSerArg
*****Arg*****AlaGlyGlySerTyrValTyrLeuSerCysPheCys***AlaGly
ATTAATAAAGATGATAGGCCGGTGGCAGCTACGTTTACCTATCCTGTTTTTGTTAAGCCG~~

5000

AlaArgSerGlySerSerPheGlyValLysLysValAsnSerAlaAspGluLeuAspTyr
ArgValGlnAlaHisProSerVal***LysLysSerIleAlaArgThrAsnTrpThrThr
AlaPheArgLeuIleLeuArgCysGluLysSerGln***ArgGlyArgIleGlyLeuArg
GCGCGTTCAGGCTCATCCTTCGGTGTGAAAAAGTCAATAGCGCGGACGAATTGGACTAC

5100

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AlaIleGluSerAlaArgGlnTyrAspSerLysIleLeuIleGluGlnAlaValSerGly
GlnLeuAsnArgGlnAspAsnMetThrAlaLysSer***LeuSerArgLeuPheArgAla
Asn***IleGlyLysThrIle***GlnGlnAsnLeuAsn***AlaGlyCysPheGlyLeu
GCAATTGAATCGGCAAGACAATATGACAGCAAATCTTAATTGAGCAGGCTGTTTCGGGC

CysGluValGlyCysAlaValLeuGlyAsnSerAlaAlaLeuValValGlyGluValAsp
ValArgSerValValArgTyrTrpGluThrValProArg***LeuLeuAlaArgTrpThr
***GlyArgLeuCysGlyIleGlyLysGlnCysArgValSerCysTrpArgGlyGlyPro
TGTGAGGTCGGTTGTGCGGTATTGGGAAACAGTGCCGCGTTAGTTGTTGGCGAGGTGGAC

5200

GlnIleArgLeuGlnTyrGlyIlePheArgIleHisGlnGluValGluProGluLysGly
LysSerGlyCysSerThrGluSerPheValPheIleArgLysSerSerArgLysLysAla
AsnGlnAlaAlaValArgAsnLeuSerTyrSerSerGlySerArgAlaGlyLysArgLeu
CAAATCAGGCTGCAGTACGGAATCTTTCGTATTCATCAGGAAGTCGAGCCGGA AAAAGGC

SerGluAsnAlaValIleThrValProAlaAspLeuSerAlaGluGluArgGlyArgIle
LeuLysThrGlnLeu***ProPheProGlnThrPheGlnGlnArgSerGluAspGlyTyr
***LysArgSerTyrAsnArgSerArgArgProPheSerArgGlyAlaArgThrAspThr
TCTGAAAACGCAGTTATAACCGTTCCCGCAGACCTTTCAGCAGAGGAGCGAGGACGGATA

5300

GlnGluThrAlaLysLysIleTyrLysAlaLeuGlyCysArgGlyLeuAlaArgValAsp
ArgLysArgGlnLysLysTyrIleLysArgSerAlaValGluVal***ProValTrpIle
GlyAsnGlyLysLysAsnIle***SerAlaArgLeu***ArgSerSerProCysGlyTyr
CAGGAAACGGCAAAAAAATATATAAAGCGCTCGGCTGTAGAGGTCTAGCCCGTGTGGAT

5400

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MetPheLeuGlnAspAsnGlyArgIleValLeuAsnGluValAsnThrLeuProGlyPhe
CysPheTyrLysIleThrAlaAlaLeuTyr***ThrLysSerIleLeuCysProValSer
ValPheThrArg***ArgProHisCysThrGluArgSerGlnTyrSerAlaArgPheHis
ATGTTTTTACAAGATAACGGCCGCATTGTACTGAACGAAGTCAATACTCTGCCCGGTTTC

ThrSerTyrSerArgTyrProArgMetMetAlaAlaAlaGlyIleAlaLeuProGluLeu
ArgHisThrValValIleProVal***TrpProLeuGlnValLeuHisPheProAsn***
ValIleGlnSerLeuSerProTyrAspGlyArgCysArgTyrCysThrSerArgThrAsp
ACGTCATACAGTCGTTATCCCCGTATGATGGCCGCTGCAGGTATTGCACTTCCCGAACTG

5500

IleAspArgLeuIleValLeuAlaLeuLysGly*****AlaTrpLys***AspLeuLeu
LeuThrAla***SerTyr***Arg***ArgGlyAspLysHisGlyAsnArgIleTyrPhe
***ProLeuAspArgIleSerValLysGlyValIleSerMetGluIleGlyPheThrPhe
ATTGACCGCTTGATCGTATTAGCGTTAAAGGGGTGATAAGCATGGAAATAGGATTTACTT

Phe***MetLys***TyrThrValPheValGlyThrLeuAsnMetProLeuGlyIleIle
PheArg***AsnSerThrArgCysSerLeuGlyArg***IleCysHisLeuGly***Phe
LeuAspGluIleValHisGlyValArgTrpAspAlaLysTyrAlaThrTrpAspAsnPhe
TTTTAGATGAAATAGTACACGGTGTTTCGTTGGGACGCTAAATATGCCACTTGGGATAATT

5600

SerProGluAsnArgLeuThrValMetLys***IleAlaLeu***GlyHisThrSerTrp
HisArgLysThrGly***ArgLeu***SerLysSerHisCysArgAspIleArgValGly
ThrGlyLysProValAspGlyTyrGluValAsnArgIleValGlyThrTyrGluLeuAla
TCACCGGAAAACCGGTTGACGGTTATGAAGTAAATCGCATTGTAGGGACATACGAGTTGG

5700

29/69

LeuAsnArgPhe***ArgGlnLysAsnTrpLeuLeuProLysGlyThrAspCysPheTyr
***IleAlaPheGluGlyLysArgThrGlyCysTyrProArgValArgIleAlaSerMet
GluSerLeuLeuLysAlaLysGluLeuAlaAlaThrGlnGlyTyrGlyLeuLeuLeuTrp
CTGAATCGCTTTTGAAGGCAAAAGAACTGGCTGCTACCCAAGCGTACGGATTGCTTCTAT

GlyThrValThrValLeuSerValLeu***ThrValLeuCysAsnGlyLeuHisSerArg
GlyArgLeuProSer***AlaCysCysLysLeuPheTyrAlaMetGlyCysThrAlaGly
AspGlyTyrArgProLysArgAlaValAsnCysPheMetGlnTrpAlaAlaGlnProGlu
GGGACGGTTACCGTCCTAAGCGTGCTGTAACTGTTTTATGCAATGGGCTGCACAGCCGG

5800

LysIleThr***GlnArgLysValIleIleProIleLeuThrGluLeuArg***PheGln
Lys***ProAspLysGlyLysLeuLeuSerGlnTyr***ProAsn***AspAspPheLys
AsnAsnLeuThrLysGluSerTyrTyrProAsnIleAspArgThrGluMetIleSerLys
AAAATAACCTGACAAAGGAAAGTTATTATCCCAATATTGACCGAACTGAGATGATTTCAA

LysAspThrTrpLeuGlnAsnGlnAlaIleAlaAlaAlaValProLeuIleLeuArgPhe
ArgIleArgGlyPheLysIleLysPro***ProArgGlnCysHis***SerTyrAlaLeu
GlyTyrValAlaSerLysSerSerHisSerArgGlySerAlaIleAspLeuThrLeuTyr
AAGGATACGTGGCTTCAAAATCAAGCCATAGCCGCGGCAGTGCCATTGATCTTACGCTTT

5900

IleAsp***ThrArgValSerLeuTyrGlnTrpGlyAlaAspLeuIleLeuTrpMetAsn
SerIleArgHisGly***AlaCysThrAsnGlyGluProIle***PheTyrGly***Thr
ArgLeuAspThrGlyGluLeuValProMetGlySerArgPheAspPheMetAspGluArg
ATCGATTAGACACGGGTGAGCTTGTACCAATGGGGAGCCGATTGATTTTATGGATGAAC

6000

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AlaLeuIleMetArgGlnMetGluTyrHisAlaMetLysArgLysIleAlaAspValCys
 LeuSerSerCysGlyLysTrpAsnIleMetGln***SerAlaLysSerGlnThrPheAla
 SerHisHisAlaAlaAsnGlyIleSerCysAsnGluAlaGlnAsnArgArgArgLeuArg
 GCTCTCATCATGCGGCAAATGGAATATCATGCAATGAAGCGCAAATCGCAGACGTTTGC

AlaProSerTrpLysThrValGlyLeuLysHisIleAlaSerAsnGlyGlyThrMetTyr
 LeuHisHisGlyLysGlnTrpVal***SerIle***ProArgMetValAlaLeuCysIle
 SerIleMetGluAsnSerGlyPheGluAlaTyrSerLeuGluTrpTrpHisTyrValLeu
 GCTCCATCATGGAAAACAGTGGGTTTGAAGCATATAGCCTCGATGGTGGCACTATGTAT

6100

***GluThrAsnHisThrProIleAlaIleLeuIleSerProLeuAsnLysLeuLeuThr
 LysArgArgThrIleProGln***LeuPhe***PheProArg***IleAsnPhe***Pro
 ArgAspGluProTyrProAsnSerTyrPheAspPheProValLys***ThrPheAsnArg
 TAAGAGACGAACCATACCCCAATAGCTATTTTGATTTCCTTAAATAAACTTTTAACC

ValAlaArgThrAsnTyrIleSer***LeuPheArgGlnGluThrArgArgMet***Leu
 LeuHisGlyGlnThrIle***AlaAsnSerPheGlyArgLysProAspValCysAsnTrp
 CysThrAspLysLeuTyrLysLeuThrLeuSerAlaGlyAsnProThrTyrValThrGly
 GTTGACGACAACTATATAAGCTAACTCTTTCGGCAGGAACCCGACGTATGTAAGT

6200

ValLeuArgGluPheIleTyrSerArg***Tyr***ArgCysLysAlaGluArgTyrCys
 PheLeuGlyAsnLeuTyrIleValAspSerIleGluAspValArgGlnSerAspIleAla
 Ser***GlyIleTyrIle*****IleValLeuLysMet***GlyArgAlaIleLeuArg
 GTTCTTAGGGAATTTATATATAGTAGATAGTATTGAAGATGTAGGCAGAGCGATATTGC

6300

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GlyHisTyrLeuArgAlaLeuArgGlnAspSerLeuIleIleArgLeuIleAla***Arg
ValIleIleCysValArgCysGlyLysIleAla*****Asp***SerHisArgGly
SerLeuSerAlaCysAlaAlaAlaArg***ProAspAsnLysThrAspArgIleGluGly
GGTCATTATCTGCGTGCGCTGCGGCAAGATAGCCTGATAATAAGACTGATCGCATAGAGG

GlyGlyIleSerHisArgProLeuSerThrGlySerSerAlaSerLeuAsnSerAlaTrp
ValValPheHisThrAlaHisCysGlnGlnAlaValGlnPrcArg***IleGlnHisGly
TrpTyrPheThrProProIleValAsnArgGlnPheSerLeuValLysPheSerMetGly
GGTGGTATTTACACCGCCCATTTGTCAACAGGCAGTTCAGCCTCGTTAAATTCAGCATGG

6400

ValSerLeuMetLysIleHisLeuHisTrp*****IleGln***GlyGluIle
TyrHisLeu***LysPheIleTyrIleGlyAspAsnSerLysSerSerArgAlaLys***
IleThrTyrGluAsnSerSerThrLeuValIleIleValAsnProValGlyArgAsnAsn
GTATCACTTATGAAAATTCATCTACATTGGTGATAATAGTAAATCCAGTAGGGCGAAATA

IleAspCysAsnLeuArgGlyLysThrAlaGlnSerGlnThrArgLeuCysArgLeuArg
LeuThrValIleTyrGlyAlaLysArgHisAsnLeuLysArgAspCysAlaVal***Gly
LeuPheThrGlyGlnAsnGlyThrIleSerAsnGluIleValProPheLysGly
ATTGACTGTAATTTACGGGGCAAACGGCACAAATCTCAAACGAGATTGTGCCGTTTAAGG

6500

GlyArgPhe***LysTyrPheIleLeuProThrIle***LeuArgArgArgLeuLysMet
GluAspSerArgAsnIleSerTyrPheGlnLeuTyrSer***GlyGlyAsp***Lys***
LysIleLeuGluIlePheHisThrSerAsnTyrIleValLysGluGluThrGluAsnGlu
GGAAGATTCTAGAAATATTTCACTTCCAACATATAGTTAAGGAGGAGACTGAAAATG

6600

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LysLysLeuPhePheLeuLeuLeuLeuL uPheLeuIleTyrLeuGlyTyrAspTyrVal
ArgSerCysPhePheTyrCysTyrCysTyrSer***TyrThr***ValMetThrThrLeu
GluValValPhePheIleValIleValIleLeuAsnIleLeuArgLeu***LeuArg***
AAGAAGTTGTTTTTTTATTGTTATTGTTATTCTTAATATACTTAGGTTATGACTACGTT

AsnGluAlaLeuPheSerGlnGluLysValGluPheGlnAsnTyrAspGlnAsnProLys
MetLysHisCysPheLeuArgLysLysSerAsnPheLysIleMetIleLysIleProLys
SerThrValPheSerGlyLysSerArgIleSerLysLeuSerLysSerGlnArg
AATGAAGCACTGTTTTCTCAGGAAAAGTCGAATTTCAAATATGATCAAATCCCAA

6700

GluHisLeuGluAsnSerGlyThrSerGluAsnThrGlnGluLysThrIleThrGluGlu
AsnIle***LysIleValGlyLeuLeuLysIleProLysArgLysGlnLeuGlnLysAsn
ThrPheArgLys***TrpAspPhe***LysTyrProArgGluAsnAsnTyrArgArgThr
GAACATTTAGAAAATAGTGGGACTTCTGAAAATACCCAAGAGAAACAATTACAGAAGAA

GlnValTyrGlnGlyAsnLeuLeuLeuIleAsnSerLysTyrProValArgGlnGluVal
ArgPheIleLysGluIleCysTyr***SerIleValAsnIleLeuPheAlaLysLysCys
GlyLeuSerArgLysSerAlaIleAsnGln*****IleSerCysSerProArgSerVal
CAGGTTTATCAAGGAAATCTGCTATTAATCAATAGTAAATATCCTGTTCCCAAGAAGTG

6800

SerGlnIleSerIleTyrLeuAsnMetThrAsn*****MetAspThrGlyCys
GluValArgTyrArgGluPheIle***Thr***ArgIleAsnLysTrpIleArgValAla
LysSerAspIleValAsnLeuSerLysHisAspGluLeuIleAsnGlyTyrGlyLeuLeu
TGAAGTCAGATATCGTGAATTTATCTAAACATGACGAATTAATAAATGGATACGGGTTGC

6900

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LeuIleValIlePheIleCysGlnLysLys***HisLysAsnPheGlnArgTrpSerMet
*****TyrLeuTyrValLysArgAsnSerThrLysIlePheArgAspGlyGln***
AspSerAsnIleTyrMetSerLysGluIleAlaGlnLysPheSerGluMetValAsnAsp
TTGATAGTAATATTTATATGTCAAAGAAATAGCACAAAATTTTCAGAGATGGTCAATG

MetLeu***ArgValAlaLeuValIleLeuLeuLeuIleValAlaIleGluThrLeuMet
CysCysLysGlyTrpArg***SerPheTyrTyr*****TrpLeuSerArgLeu*****
AlaValLysGlyGlyValSerHisPheIleIleAsnSerGlyTyrArgAspPheAspGlu
ATGCTGTAAAGGGTGGCGTTAGTCATTTTATTATTAATAGTGGCTATCGAGACTTTGATG

7000

SerLysValCysPheThrLysLysTrpGlyLeuSerMetProTyrGlnGlnValIleVal
AlaLysCysAlaLeuProArgAsnGlyGly***ValCysLeuThrSerArgLeu*****
GlnSerValLeuTyrGlnGluMetGlyAlaGluTyrAlaLeuProAlaGlyTyrSerGlu
AGCAAAGTGTGCTTTACCAAGAAATGGGGGCTGAGTATGCCTTACCAGCAGGTTATAGTG

SerIleIleGlnValTyrHis***Met***AspGlnAla***ArgLysTrpAsnGluPro
Ala***PheArgPheIleThrArgCysArgIleLysLeuAspGluAsnGlyThrSerPro
HisAsnSerGlyLeuSerLeuAspValGlySerSerLeuThrLysMetGluArgAlaPro
AGCATAATTCAGGTTTATCACTAGATGTAGGATCAAGCTTGACGAAAATGGAACGAGCCC

7100

LeuLysGluSerGly***LysLysMetLeuGlyAsnThrGlySerPheTyrValIleGln
***ArgLysValAspArgArgLysCysLeuGluIleArgValHisPheThrLeuSerArg
GluGlyLysTrpIleGluGluAsnAlaTrpLysTyrGlyPheIleLeuArgTyrProGlu
CTGAAGGAAAGTGGATAGAAGAAAATGCTTGGAAATACGGGTTTATTTACGTTATCCAG

7200

000000-000000

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ArgThrLysGlnSer***GlnGluPhe

GlyGlnAsnArgValAsnArgAsnSer

AspLysThrGluLeuThrGlyIleGln

AGGACAAAACAGAGTTAACAGGAATTC

7227

FIGURE 6 (1/2)

ECORV

GATATCGTTACGCTTCATGTGCCGCTCAATACGGATACGGACTATATATCAGCCACGACAAA 64
TACAGAGAAATGAAGCAAGGAGCATTTCTTATCAATACTGGCGGCTCCACTTGTAGATACCTATGAGTTGGTTAAAGCATAGAAAAACGG 155
GAAACTGGCGGTCCGTCATTGGATGTATTGGAAGGAGAGAGATTTTCTACTCTGTATTGACCCCAAAAACCAATTGATAATCAATTT 246
TTACTTAAACTTCAAAGAATGCCTAAACGTGATAATCACACCCGATACCGGCTTATTATACCGAGCAAGCGTTCGGTGATACCGTTGAAAAAA 337
RBS **▼** MET ASN ARG ILE LYS VAL ALA ILE LEU PHE GLY CYB
HaeIII
CCATTAAAAACTGTTGGATTGTTGAAAGGAGACAGGAGC ATG AAT AGA ATA AAA GTT GCA ATA CTG TTT GGG GGT TGC 415
NlaIII
SER GLU GLU HIS ASP VAL SER VAL LYS SER ALA ILE GLU ILE ALA ALA ASN ILE ASN LYS GLU LYS TYR
TCA GAG GAG AAT GAC GTA TCG GTA AAA TCT GCA ATA GAG ATA GCC GCT AAC AAT AAT AAA GAA AAA TAC 484
GLU PRO LEU TYR ILE GLY ILE THR LYS SER GLY VAL TRP LYS MET CYB GLU LYS PRO CYB ALA GLU TRP
GAG CCG TTA TAC ATT GGA ATT ACG AAA TCT GGT GTA TGG AAA ATG TGC GAA AAA CCT TGC GCG GAA TGG 553
GLU ASN ASP ASN CYB TYR SER ALA VAL LEU SER PRO ASP LYS LYS MET HIS GLY LEU LEU VAL LYS LYS
GAA AAC GAC AAT TGC TAT TCA GCT GTA CTC TCG CCG GAT AAA AAA ATG CAC GGA TTA CTT GTT AAA AAG 622
ASN HIS GLU TYR GLU ILE ASN HIS VAL ASP VAL ALA PHE SER ALA LEU HIS GLY LYS SER GLY GLU ASP
AAC CAT GAA TAT GAA ATC AAC CAT GAT GTA GCA TTT TCA GCT TTG CAT GGC AAG TCA GGT GAA GAT 691
GLY SER ILE GLN GLY LEU PHE GLU LEU SER GLY ILE PRO PHE VAL GLY CYB ASP ILE GLN SER SER ALA
GGA TCC ATA CAA GGT CTG TTT GAA TTG TCC GGT ATC CCT TTT GTA GGC TGC GAT ATT CAA AGC TCA GCA 760
ILE CYB MET ASP LYS SER LEU THR TYR ILE VAL ALA LYS ASN ALA GLY ILE ALA THR PRO ALA PHE TRP
ATT TGT ATG GAC AAA TCG TTG ACA TAC ATC GTT GCG AAA AAT GCT GGG ATA GCT ACT CCC GCC TTT TGG 829
VAL ILE ASN LYS ASP ASP ARG PRO VAL ALA ALA THR PHE THR TYR PRO VAL PHE VAL LYS PRO ALA ARG
GTT ATT AAT AAA GAT GAT AGG CCG GTG GCA GCT ACC TAT CCT GTT TTT AAG CCG GCG CGT 898

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FIGURE 6 (2/2)

SER GLY SER SER PHE GLY VAL LYS LYS VAL ASN SER ALA ASP GLU LEU ASP TYR ALA ILE GLU SER ALA
 TCA GGC TCA TCC TTC GGT GTG AAA AAA GTC AAT AGC GCG GAC GAA TTG GAC TAC GCA ATT GAA TCG GCA 967

 ARG GLN TYR ASP SER LYS ILE LEU ILE GLU GLN ALA VAL SER GLY CYB GLU VAL GLY CYB ALA VAL LEU
 AGA CAA TAT GAC AGC AAA ATC TTA ATT GAG CAG GCT GTT TCG GGC TGT GAG GTC GGT TGT GCG GTA TTG 1036

 GLY ASN SER ALA ALA LEU VAL VAL GLY GLU VAL ASP GLN ILE ARG LEU GLN TYR GLY ILE PHE ARG ILE
 GGA AAC AGT GCC GCG TTA GTT GGT GGC GAG GAG GTG GAC CAA ATC AGG CTG CAG TAC GGA ATC TTT CGT ATT 1105

 HIS GLN GLU VAL GLU PRO GLU LYS GLY SER GLU ASN ALA VAL ILE THR VAL PRO ALA ASP LEU SER ALA
 CAT CAG GAA GTC GAG CCG GAA AAA GGC TCT GAA AAC GCA GTC ATA ACC GTT CCC GCA GAC CTT TCA GCA 1174

 GLU GLU ARG GLY ARG ILE GLN GLU THR ALA LYS LYS ILE TYR LYS ALA LEU GLY CYB ARG GLY LEU ALA
 GAG GAG CGA GGA CGG ATA CAG GAA ACG GCA AAA ATA TAT AAA GCG CTC GGC TGT AGA GGT CTA GCC 1243

 ARG VAL ASP MET PHE LEU GLN ASP ASN GLY ARG ILE VAL LEU ASN GLU VAL ASN THR LEU PRO GLY PHE
 CGT GTG GAT ATG TTT TTA CAA GAT AAC GGC CGC ATT GTA CTG AAC GAA GTC AAT ACT CTG CCC GGT TTC 1312

 THR SER TYR SER ARG TYR PRO ARG MET MET ALA ALA ALA GLY ILE ALA LEU PRO GLU LEU ILE ASP ARG
 ACG TCA TAC AGT CGT TAT CCC CGT ATG ATG GCT GCA GGT ATT GCA CTT CCC GAA CTG ATT GAC CGC 1381

 LEU ILE VAL LEU ALA LEU LYS GLY *** ***
 TTG ATC GTA TTA TTA GCG TTA AAG GGG TGA TAA GCATGGAAATAGGATTACTTTTTTAGATGAAATAGTACACGGTTCGTT 1462
 NlaIII
 GGGACGCTAAATATGCCACTTGGGATAATTTACCCGGAAAAACCGGTTGACGGTTATGAAGTAAATCGCATTTGTAGGGACATACGAGTTGGC 1553
 TGAATCGCTTTTGAAGGCCAAAGAACTGGCTGCTACCCAAAGGGTACGGATTGCTTCTATGGACGGTTACCGTCTTAAGCGTGTGTAAC 1644
 TGTTTTATGCAATGGGCTGCACAGCCGGAAAAATAACCTGACAAAGGAAAGTTATTATCCCAATATTGACCGAACTGAGATGATTTCAAAAG 1735

 SacII
 GGATACGTGGCTTCAAAATCAAGCCATAGCCGCG 1769

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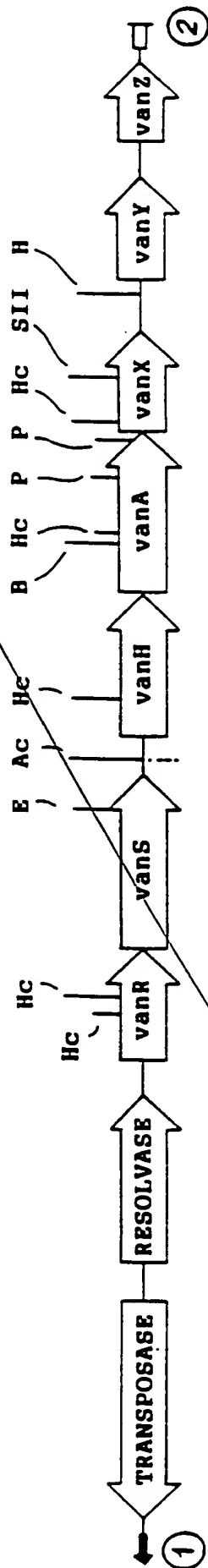


FIG. 7 a

660220" 522360

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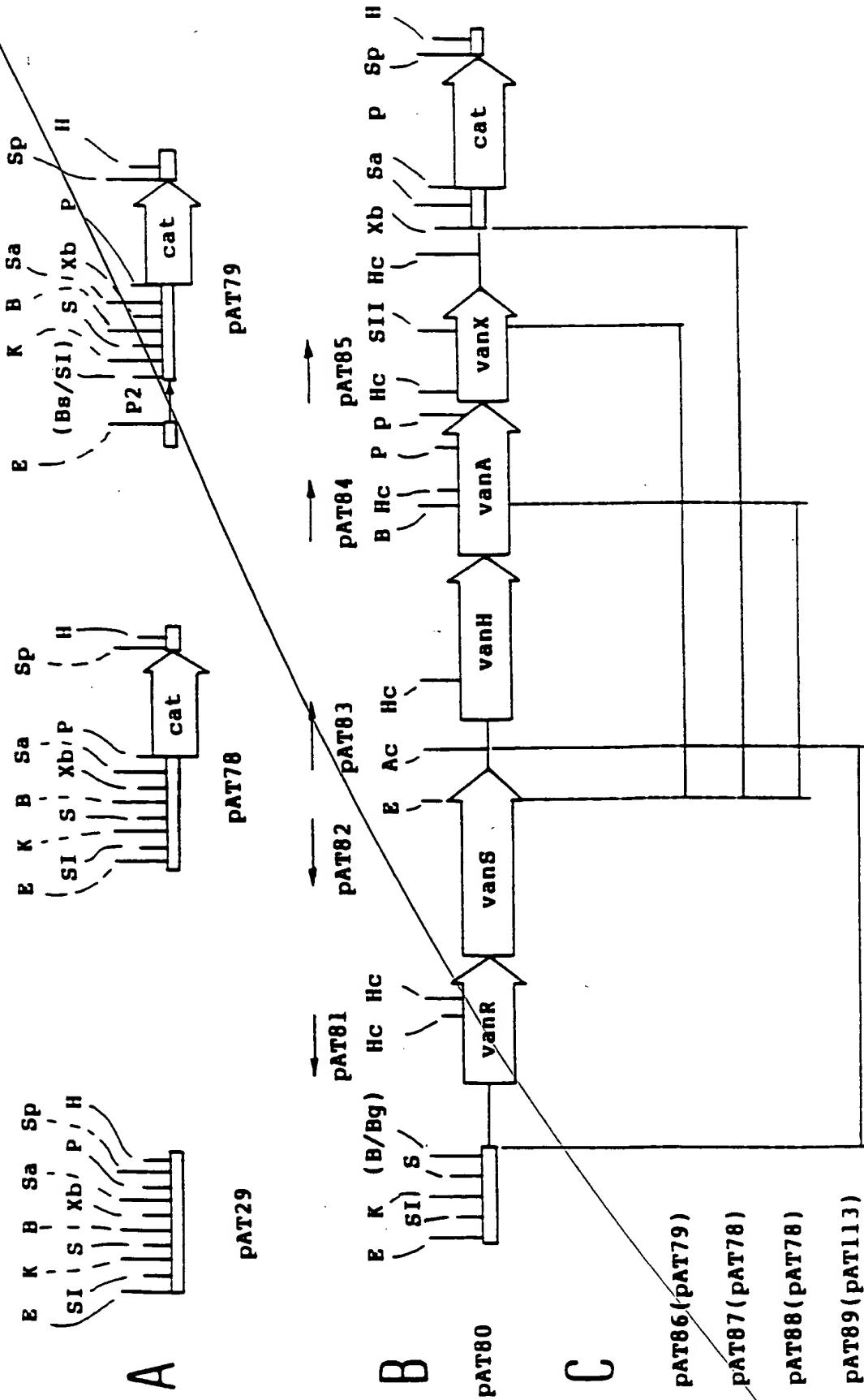


FIG. 7b

FIGURE 8 (1/23)

1	GGG	GTA	GCG	TCA	GGA	AAA	TGC	GGA	TTT	ACA	ACG	CTA	AGC	CTA	TTT	TCC	TGA	CGA	ATC	CCT
61	CGT	TTT	TAA	CAA	CGT	TAA	GAA	AGT	TTT	AGT	GGT	CTT	AAA	GAA	TTT	AAT	GAG	ACT	ACT	TTC
121	TCT	GAG	TTA	AAA	TGG	TAT	TCT	CCT	AGT	AAA	TTA	ATA	TGT	TCC	CAA	CCT	AAG	GGC	GAC	ATA
181	TGG	TGT	AAC	AAA	TCT	TCA	TTA	AAG	CTA	CCT	GTC	CGT	TTT	TTA	TAT	TCA	ACT	GCT	GTT	GTT
241	AGG	TGG	AGA	GTA	TTC	CAA	ATA	CTT	ATA	GCA	TTG	ATA	ATT	ATG	TTT	AAA	GCA	CTG	GCT	CTT
301	TGC	AAT	TGA	TGC	TGT	ATG	GTG	CGT	TCT	CTA	AGC	TCA	CCT	TGT	TTT	CCG	AAG	AAA	ATA	GCT
361	CTT	GCC	AAT	CCA	TTC	ATG	GCT	TCT	CCT	TTA	TTC	AAT	CCT	CTT	TGT	ATT	TTT	CTT	CTT	AAT
421	GAT	TCA	TEC	GAT	ATA	TAA	TTC	AAA	ATA	AAG	ATC	GTT	TTT	TCT	ATT	CGG	CCC	ATC	TCA	CGT
481	AAG	GCT	GTA	GCT	AAG	CTG	TTT	TGT	CTT	GAA	TAG	GAA	CCT	AGC	TTC	CCC	ATA	ATA	AGG	GAT
541	GCT	GAA	ACT	GTT	CCC	TCC	CTT	ATA	GAA	TGA	GCT	AAT	CGC	AAA	ACA	TCC	TCA	TAA	TTT	TCT
601	TTA	ATG	ACC	TTT	GTA	TTT	ATT	TGT	CCA	CGT	AAA	ATG	GCT	TCT	AGT	TTT	GGA	TAC	TCA	CTT

661 TTA TCT ATC GTA AAT AAT TTT GAG TCC GAT AAA TCC CTT ATT CTT GGG GCA AAT TTA
 GCT TTA TCT ATC GTA AAT AAT TTT GAG TCC GAT AAA TCC CTT ATT CTT GGG GCA AAT TTA
 721 AAT CCT AAT AAA TGA GTC AGT CCG AAT ATT TGG TCA GTG TAA CCG GCA GTG TCT GTA TAA
 AAT CCT AAT AAA TGA GTC AGT CCG AAT ATT TGG TCA GTG TAA CCG GCA GTG TCT GTA TAA
 781 TGT TCC TCT ATG TTT AGA TCC GTC TCA TGA TGT AAC AAA CCA TCC AAA ACA TGA ATC GCA
 TGT TCC TCT ATG TTT AGA TCC GTC TCA TGA TGT AAC AAA CCA TCC AAA ACA TGA ATC GCA
 841 TCT CTT GAA TTA GTA TGA ATA ATC TTT GTG TAG TAA GAA GAG AAT TGA TCA CTT GTA AAT
 TCT CTT GAA TTA GTA TGA ATA ATC TTT GTG TAG TAA GAA GAG AAT TGA TCA CTT GTA AAT
 901 CGG TAG ATG GTG GCT CCT TTT CCA GTT CCA TAA TGT GGA TTT GCA TCT GCA TGT AGT GAT
 TCT CTT GAA TTA GTA TGA ATA ATC TTT GTG TAG TAA GAA GAG AAT TGA TCA CTT GTA AAT
 961 GAA ACA CCT AGC TGC ATT CTC ATA CCA TCT GAC GAA GAT GTT GTA CCG TCG CCC CAA TAG
 GAA ACA CCT AGC TGC ATT CTC ATA CCA TCT GAC GAA GAT GTT GTA CCG TCG CCC CAA TAG
 1021 AAA GGC AAT TGT AAT TTA TGA TGA AAG TTT ACT AAT ATG GCT TGG GCT TTA TTC ATG GCA
 AAA GGC AAT TGT AAT TTA TGA TGA AAG TTT ACT AAT ATG GCT TGG GCT TTA TTC ATG GCA
 1081 TCT TCA TAC ATG CGC CAT TGA GAT ACA TTT GCT AGT TGC TTA TAT GTA AGT CCG GGT GTG
 TCT TCA TAC ATG CGC CAT TGA GAT ACA TTT GCT AGT TGC TTA TAT GTA AGT CCG GGT GTG
 1141 GCT TCG GCC ATC TTG CTC AAG CCA ATA TTC ATT CCC ATT CCT AAA AGG GCA GCC ATG ATA
 GCT TCG GCC ATC TTG CTC AAG CCA ATA TTC ATT CCC ATT CCT AAA AGG GCA GCC ATG ATA
 1201 ATG ATT GTT TCT TCC TTA TCT TCT GGT TTT CGA TTA TTG GAA GCA TGA GTG AAT TGC TCA TGA
 ATG ATT GTT TCT TCC TTA TCT TCT GGT TTT CGA TTA TTG GAA GCA TGA GTG AAT TGC TCA TGA
 1261 AAT CCT GTT ATA TGG GCC ACA TCC ATG AGT AAA TCA GTT AAT TTT ATT CTT GGT AGC ATC
 AAT CCT GTT ATA TGG GCC ACA TCC ATG AGT AAA TCA GTT AAT TTT ATT CTT GGT AGC ATC
 1321 TGA TAA AGG CTT GCA CTA AAT TTT TTT GCT TCT TCT GGA ACA TCT TTT TCT AAG CGT GCA
 TGA TAA AGG CTT GCA CTA AAT TTT TTT GCT TCT TCT GGA ACA TCT TTT TCT AAG CGT GCA
 1381 AGT GAT AGC TTT CCT TTT TCA AGA GAA ACC CCA TCT AAC TTA TTG GAA TTG GCA GCT AAC
 AGT GAT AGC TTT CCT TTT TCA AGA GAA ACC CCA TCT AAC TTA TTG GAA TTG GCA GCT AAC
 1441 CAC TTT AAC CTT TCA TTA AAG CTG GTT CTC TCC GTT ATA TAA TCT TCG AAT GAT AAA
 CAC TTT AAC CTT TCA TTA AAG CTG GTT CTC TCC GTT ATA TAA TCT TCG AAT GAT AAA

FIGURE 8 (3/23)

1501 ACT GAT AAT CTC GTA TTC CCC TTC GAT TGA TTC CAT GTA TCT TCC GAA AAC AAA TAT
 1561 TCC TCA AAA TCC CTA TAT TGT CTG CCA ACA ATG GAA ACA TCT CCT GCC CGA ACA TGC
 1621 TCC CGA AGT TCT GTT AAA ACA GCC ATT TCA TAG TAA TGA CGA TTA ATT GTT GTA CCA TCA
 1681 TCC TCG TAT AAA TGT CTT TTC CAT CGT TTT GAA ATA AAA TCC ACA GGT GAG TCA TCA GGC
 1741 ACT TTT CGC TTT CCA GAT TCG TTC ATT CCT CGG ATA ATC TCA ACA GCT TGT AAA AGT GGC
 1801 TCA TTT GCC TTT GTA GAA TGA AAT TCC AAT ACT CTT AAT AGC GTT GGC GTA TAT TTT CTT
 1861 AGT GAA TAA AAC CGT TTT TGC AGT AAG TCT AAA TAA TCA TAG TCG GCA GGA CGT GCA AGT
 1921 TCC TGA GCC TCT TCT ACT GAA GAG ACA AAG GTA TTC CAT TCA ATA ACC GAT TCT AAA ACC
 1981 TTA AAA ACG TCT AAT TTT TCC TCT CTT GCT TTA ATT AAT GCT TGT CCG ATG TTC GTA AAG
 2041 TGT ATA ACT TTC TCA TTT AGC TTT TTA CCG TTT TGT TTC TGG ATT TCC TCT TGA GCC TTA
 2101 CGA CCT TTT GAT AAC AAA CTA AGT ATT TGC CTA TCA TGA ATT TCA AAC GCT TTA TCC GTT
 2161 AGC TCC TGA GTA AGT TGT AAT AAA TAG ATG GTT AAT ATC GAA TAA CGT TTA TTT TCT TGA
 2221 AAG TCA CGG AAT GCA TAC GGC TCG TAT CTT GAG CCT AAG CGA GAC AGC TGC AAC AGG CGG
 2281 TTA CGG TGC AAA TGA CTA ATT TGC ACT GTT TCT AAA TCC ATT CCT CGT ATG TAT TCG AGT
 2341

FIGURE 8 (4/23)

CGT TCT ATT ATT TTT AGA AAA GTT TCG GGT GAA GGA TGA CCC GGT GGC TCT TTT AAC CAA
2401
CCC AAT ATC GTT TTA TTG GAT TCG GAT GGA TGC TGC GAG GTA ATA ATC CCT TCA AGC TTT
2461
TCT TTT TGC TCA TTT GTT AGA GAT TTA CTA ACC GTA TTA AAT AGC TTC TTT TCA GCC ATT
2521
GCC CTT GCT TCC CAC ACC ATT CTT TCA AGT GTA GTG ATA GCA GGC AGT ATA ATT TTG TTT
2581
TTT CTT AGA AAA TCT ATG CAT TCA TGC AGT AGA TGA ATG GCA TCA CCA TTT TCC AAA GCT
2641
AAT TGA TGA AGG TAC TTA AAT TTC AAA TGA TCC CAA AGT GTA TAT TCA CTC AGG GTA AAA GTT ACA AAG TCG
2701
TAT TCA CTT CGA ATT TCT TTC AAA TGA TCC CAA AGT GTA TTT TCC CTT TGA GGA TAA TGA
2761
TCA AGC GAG GAT GGA CTA ACA CCA ATC TGT TTC GAT ATA TAT TGT ATG ACC GAA TCT GGG
2821
ATG CTT TTG ATA TGA GTG TAT GGC CAA CCG GGA TAC CGA AGA ACA GCT AAT TGA ACA GCA
2881
AAT CCT AAA CGG TTT TCT TCC CTC CTT CGC TTA TTA ACT ATT TCT AAA TCC CGT TTG GAA
2941
AAA GTG AAG TAG GTC CCC AGT ATC CAT TCA TCT TCA GGG ATT TGC ATA AAA GCC TGT CTC
3001
TGT TCC GGT GTA AGC AAT TCT CTA CCT CTC GCA ATT TTC ATT CAG TAT CAT TCC ATT TCT
3061
GTA TTT TCA ATT TAT TAG TTC AAT TAT ATA TCA ATA GAG TGT ACT CTA TTG ATA CAA ATG
3121
TAG TAG ACT GAT AAA ATC ATA GTT AAG AGC GTC TCA TAA GAC TTG TCT CAA AAA TGA GGT

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FIGURE 8 (5/23)

3181 **résolvase**
 LEU ARG LYS ILE GLY TYR ILE ARG VAL SER SER THR ASN GLN ASN PRO SER ARG
 GAT ATT TTG CCG AAA ATC GGT TAT ATT CGT GTC AGT TCG ACT AAC CAG AAT CCT TCA AGA

3241
 GLN PHE GLN GLN LEU ASN GLU ILE GLY MET ASP ILE ILE TYR GLU GLU LYS VAL SER GLY
 CAA TTT CAG CAG TTG AAC GAG ATC GGA ATG GAT ATT ATA TAT GAA GAG AAA GTT TCA GGA

3301
 ALA THR LYS ASP ARG GLU GLN LEU GLN LYS VAL LEU ASP ASP LEU GLN GLU ASP ASP ILE
 GCA ACA AAG GAT CGC GAG CAA CTT CAA AAA GTG TTA GAC GAT TTA CAG GAA GAT GAC ATC

3361
 ILE TYR VAL THR ASP LEU THR ARG ILE THR ARG SER THR GLN ASP LEU PHE GLU LEU ILE
 ATT TAT GTT ACA GAC TTA ACT CGA ATC ACT CGT AGT ACA CAA GAT CTA TTT GAA TTA ATC

3421
 ASP ASN ILE ARG ASP LYS LYS ALA SER LEU LYS SER LEU LYS ASP THR TRP LEU ASP LEU
 GAT AAC ATA CGA GAT AAA AAG GCA AGT TTA AAA TCA CTA AAA GAT ACA TGG CTT GAT TTA

3481
 SER GLU ASP ASN PRO TYR SER SER GLN PHE LEU ILE THR VAL MET ALA GLY VAL ASN GLN LEU
 TCA GAA GAT AAT CCA TAC AGC CAA TTC TTA ATT ACT GTA ATG GCT GGT GGT AAC CAA TTA

3541
 GLU ARG ASP LEU ILE ARG MET ARG GLN ARG GLU GLY ILE GLU LEU ALA LYS LYS GLU GLY
 GAG CGA GAT CTT ATT CGG ATG AGA CAA CGT GAA GGG ATT GAA TTG GCT AAG AAA GAA GGA

3601
 LYS PHE LYS GLY ARG LEU LYS LYS TYR HIS LYS ASN HIS ALA GLY MET ASN TYR ALA VAL
 AAG TTT AAA GGT CGA TTA AAG AAG TAT CAT AAA AAT CAC GCA GGA ATG AAT TAT GCG GTA

3661
 LYS LEU TYR LYS GLU GLY ASN MET THR VAL ASN GLN ILE CYS GLU ILE THR ASN VAL SER
 AAG CTA TAT AAA GAA GGA AAT ATG ACT ACT GTA AAT CAA ATT TGT GAA ATT ACT AAT GTA TCT

3721
 ARG ALA SER LEU TYR ARG LYS LEU SER GLU VAL ASN ASN
 AGG GCT TCA TTA TAC AGG AAA TTA TCA GAA GTG AAT AAT TAG CCA TTC TGT ATT CCG CTA

FIGURE 8 (6/23)

3781
ATG GGC AAT ATT TTT AAA GAA GAA AAG GAA ACT ATA AAA TAT TAA CAG CCT CCT AGC GAT
3841
GCC GAA AAG CCC TTT GAT AAA AAA AGA ATC ATC ATC TTA AGA AAT TCT TAG TCA TTT ATT
3901
ATG TAA ATG CTT ATA AAT TCG GCC CTA TAA TCT GAT AAA TTA TTA AGG GCA AAC TTA TGT
3961
VanR MET SER ASP LYS ILE LEU ILE VAL ASP ASP GLU HIS GLU ILE ALA
GAA AGG GTG ATA ACT ATG AGC GAT AAA ATA CTT ATT GTG GAT GAT GAA CAT GAA ATT GCC
4021
ASP LEU VAL GLU LEU TYR LEU LYS ASN GLU ASN TYR THR VAL PHE LYS TYR TYR THR ALA
GAT TTG GTT GAA TTA TAC TTA AAA AAC GAG AAT TAT ACG GTT TTC AAA TAC TAT ACC GCC
4081
LYS GLU ALA LEU GLU CYS ILE ASP LYS SER GLU ILE ASP LEU ALA ILE LEU ASP ILE MET
AAA GAA GCA TTG GAA TGT ATA GAC AAG TCT GAG ATT GAC CTT GCC ATA TTG GAC ATC ATG
4141
LEU PRO GLY THR SER GLY LEU THR ILE CYS GLN LYS ILE ARG ASP LYS HIS THR TYR PRO
CTT CCC GGC ACA AGC GGC CTT ACT ATC TGT CAA AAA ATA AGG GAC AAG CAC ACC TAT CCG
4201
ILE ILE MET LEU THR GLY LYS ASP THR GLU VAL ASP LYS ILE THR GLY LEU THR ILE GLY
ATT ATC ATG CTG ACC GGC AAA GAT ACA GAG GTA GAT AAA ATT ACA GGG TTA ACA ATC GGC
4261
ALA ASP ASP TYR ILE THR LYS PRO PHE ARG PRO LEU GLU LEU ILE ALA ARG VAL LYS ALA
GCG GAT GAT TAT ATA ACG AAG CCC TTT CGC CCA CTG GAG TTA ATT GCT CGG GTA AAG GCC
4321
GLN LEU ARG ARG TYR LYS LYS PHE SER GLY VAL LYS GLU GLN ASN GLU ASN VAL ILE VAL
CAG TTG CGC CGA TAC AAA AAA TTC AGT GGA GTA AAG GAG CAG AAC GAA AAT GTT ATC GTC

4381 HIS SER GLY LEU VAL ILE ASN VAL ASN THR HIS GLU CYS TYR LEU ASN GLU LYS GLN LEU
CAC TCC GGC CTT GTC ATT AAT GTT AAC ACC CAT GAG TGT TAT CTG AAC GAG AAG CAG TTA

4441 SER LEU THR PRO THR GLU PHE SER ILE LEU ARG ILE LEU CYS GLU ASN LYS GLY ASN VAL
TCC CTT ACT CCC ACC GAG TTT TCA ATA CTG CGA ATC CTC TGT GAA AAC AAG GGG AAT GTG

4501 VAL SER SER GLU LEU LEU PHE HIS GLU ILE TRP GLY ASP GLU TYR PHE SER LYS SER ASN
GTT AGC TCC GAG CTG CTA TTT CAT GAG ATA TGG GGC GAC GAA TAT TTC AGC AAG AGC AAC

4561 ASN THR ILE THR VAL HIS ILE ARG HIS LEU ARG GLU LYS MET ASN ASP THR ILE ASP ASN
AAC ACC ATC ACC GTG CAT ATC CGG CAT TTG CGC GAA AAA ATG AAC GAC ACC ATT GAT AAT

4621 PRO LYS TYR ILE LYS THR VAL TRP GLY VALGLYTYRILYSILEGLULYS
CCG AAA TAT ATA AAA ACG GTA TGG GGG GTTGGTTATAAATTGAAAAT AAA AAA AAC GAC
VANS LEUVALILELYSLEULYSASN LYS LYS ASN ASP

4682 TYR SER LYS LEU GLU ARG LYS LEU TYR MET TYR ILE VAL ALA ILE VAL VAL ALA ILE
TAT TCC AAA CTA GAA CGA AAA CTT TAC ATG ATG TAT ATC GTT GCA ATT GTT GTG GTA GCA ATT

4742 VAL PHE VAL LEU TYR ILE ARG SER MET ILE ARG GLY LYS LEU GLY ASP TRP ILE LEU SER
GTA TTC GTG TTG TAT ATT CGT TCA ATG ATC CGA GGG AAA CTT GGG GAT TGG ATC TTA AGT

4802 ILE LEU GLU ASN LYS TYR ASP LEU ASN HIS LEU ASP ALA MET LYS LEU TYR GLN TYR SER
ATT TTG GAA AAC AAC TAT GAC TTA AAT CAC CTG GAC GCG ATG AAA TTA TAT CAA TAT TCC

4862 ILE ARG ASN ASN ILE ASP ILE PHE ILE TYR VAL ALA ILE VAL ILE SER ILE LEU ILE LEU
ATA CGG AAC AAT ATA GAT ATC TTT ATT TAT GTG GCG ATT GTG ATT AGT ATT CTT ATT CTA

4922 CYS ARG VAL MET LEU SER LYS PHE ALA LYS TYR PHE ASP GLU ILE ASN THR GLY ILE ASP
TGT CGC GTC ATG CTT TCA AAA TTC GCA AAA TAC TTT GAC GAG ATA AAT ACC GGC ATT GAT

FIGURE 8 (8/23)

4982 VAL LEU ILE GLN ASN GLU ASP LYS GLN ILE GLU LEU SER ALA GLU MET ASP VAL MET GLU
 GTA CTT ATT CAG AAC GAA GAT AAA CAA ATT GAG CTT TCT TCT GCG GAA ATG GAT GTT ATG GAA
 5042 GLN LYS LEU ASN THR LEU LYS ARG THR LEU GLU LYS ARG GLU GLN ASP ALA LYS LEU ALA
 CAA AAG CTC AAC ACA TTA AAA CGG ACT CTG GAA AAG CGA GAG CAG GAT GCA AAG CTG GCC
 5102 GLU GLN ARG LYS ASN ASP VAL MET TYR LEU ALA HIS ASP ILE LYS THR PRO LEU THR
 GAA CAA AGA AAA AAT GAC GTT GTT ATG TAC TTG GCG CAC GAT ATT AAA ACG CCC CTT ACA
 5162 SER ILE ILE GLY TYR LEU SER LEU LEU ASP GLU ALA PRO ASP MET PRO VAL ASP GLN LYS
 TCC ATT ATC GGT TAT TTG AGC CTG CTT GAC GAG GCT CCA GAC ATG CCG GTA GAT CAA AAG
 5222 ALA LYS TYR VAL HIS ILE THR LEU ASP LYS ALA TYR ARG LEU GLU GLN LEU ILE ASP GLU
 GCA AAG TAT GTG CAT ATC ACG TTG GAC AAA GCG TAT CGA CTC GAA CAG CTA ATC GAC GAG
 5282 PHE PHE GLU ILE THR ARG TYR ASN LEU GLN THR ILE THR LEU THR LYS THR HIS ILE ASP
 TTT TTT GAG ATT ACA CGG TAT AAC CTA CAA ACG ATA ACG CTA ACA AAA ACG CAC ATA GAC
 5342 LEU TYR TYR MET LEU VAL GLN MET THR ASP GLU PHE TYR PRO GLN LEU SER ALA HIS GLY
 CTA TAC TAT ATG CTG GTG CAG ATG ACC GAT GAA TTT TAT CCT CAG CTT TCC GCA CAT GGA
 5402 LYS GLN ALA VAL ILE HIS ALA PRO GLU ASP LEU THR VAL SER GLY ASP PRO ASP LYS LEU
 AAA CAG GCG GTT ATT CAC GCC CCC GAG GAT CTG ACC GTG TCC GGC GAC CCT GAT AAA CTC
 5462 ALA ARG VAL PHE ASN ASN ILE LEU LYS ASN ALA ALA TYR SER GLU ASP ASN SER ILE
 GCG AGA GTC TTT AAC AAC ATT TTG AAA AAC GCC GCT GCA TAC AGT GAG GAT AAC AGC ATC

FIGURE 8 (9/23)

47/69

5522 ILE ASP ILE THR ALA GLY LEU SER GLY ASP VAL VAL SER ILE GLU PHE LYS ASN THR GLY
 ATT GAC ATT ACC GCG GGC CTC TCC GGG GAT GTG TCA ATC GAA TTC AAG AAC ACT GGA
 5582 SER ILE PRO LYS ASP LYS LEU ALA ILE PHE GLU LYS PHE TYR ARG LEU ASP ASN ALA
 AGC ATC CCA AAA GAT AAG CTA GCT GCC ATA TTT GAA AAG TTC TAT AGG CTG GAC AAT GCT
 5642 ARG SER SER ASP THR GLY GLY ALA GLY LEU GLY LEU ALA ILE ALA LYS GLU ILE ILE VAL
 CGT TCT TCC GAT ACG GGT GGC GCG GGA CTT GGA TTG GCG ATT GCA AAA GAA ATT ATT GTT
 5702 GLN HIS GLY GLY GLN ILE TYR ALA GLU SER ASN ASP THR THR THR PHE ARG VAL GLU
 CAG CAT GGA GCG CAG ATT TAC GCG GAA AGC AAT GAT AAC TAT ACG ACG TTT AGG GTA GAG
 5762 LEU PRO ALA MET PRO ASP LEU VAL ASP LYS ARG ARG SER
 CTT CCA GCG ATG CCA GAC TTG GTT GAT AAA AGG AGG TCC TAA GA GAT GTA TAT AAT TTT
 5821 TTA GGA AAA TCT CAA GGT TAT CTT TAC TTT TTC TTA GGA AAT TAA CAA TTT AAT ATT AAG
 5881 AAA CGG CTC GTT CTT ACA CGG TAG ACT TAA TAC CGT AAG AAC GAG CCG TTT TCG TTC TTC
 5941 AGA GAA AGA TTT GAC AAG ATT ACC ATT GGC ATC CCC GTT TTA TTT GGT GCC TTT CAC AGA
 6001
 VanH MET ASN ASN ILE GLY ILE THR VAL TYR GLY CYS GLU GLN ASP GLU
 AAGGTTGG TCT TAA TT ATG AAT AAC ATC GGC ATT ACT GTT TAT GGA TGT GAG CAG GAT GAG
 6063
 ALA ASP ALA PHE HIS ALA LEU SER PRO ARG PHE GLY VAL MET ALA THR ILE ILE ASN ALA
 GCA GAT GCA TTC CAT GCT CTT TCG CCT CGC TTT GGC GTT ATG GCA ACG ATA ATT AAC GCC
 6123

FIGURE 8 (10/23)

ASN VAL SER GLU SER ASN ALA LYS SER ALA PRO PHE ASN GLN CYS ILE SER VAL GLY HIS
AAC GTG TCG GAA TCC AAC GCC AAA TCC GCG CCT TTC AAT CAA TGT ATC AGT GTG GGA CAT
6183
LYS SER GLU ILE SER ALA SER ILE LEU LEU ALA LEU LYS ARG ALA GLY VAL LYS TYR ILE
AAA TCA GAG ATT TCC GCC TCT ATT CTT CTT GCG CTG AAG AGA GCC GGT GTG AAA TAT ATT
6243
SER THR ARG SER ILE GLY CYS ASN HIS ILE ASP THR THR ALA ALA LYS ARG MET GLY ILE
TCT ACC CGA AGC ATC GGC TGC AAT CAT ATA GAT ACA ACT GCT GCT AAG AGA ATG GGC ATC
6303
THR VAL ASP ASN VAL ALA TYR SER PRO ASP SER VAL ALA ASP TYR THR MET MET LEU ILE
ACT GTC GAC AAT GTG GCG TAC TCG CCG GAT AGC GTT GCC GAT TAT ACT ATG ATG CTA ATT
6363
LEU MET ALA VAL ARG ASN VAL LYS SER ILE VAL ARG SER VAL GLU LYS HIS ASP PHE ARG
CTT ATG GCA GTA CGC AAC GTA AAA TCG ATT GTG CGC TCT GTG GAA AAA CAT GAT TTC AGG
6423
LEU ASP SER ASP ARG GLY LYS VAL LEU SER ASP MET THR VAL GLY VAL GLY THR GLY
TTG GAC AGC GAC CGT GGC AAG GTA CTC AGC GAC ATG ACA GTT GGT GTG GTG GGA ACG GGC
6483
GLN ILE GLY LYS ALA VAL ILE GLU ARG LEU ARG GLY PHE GLY CYS LYS VAL LEU ALA TYR
CAG ATA GGC AAA GCG GTT ATT GAG CGG CGA CTG CGA GGA TTT GGA TGT AAA GTG TTG GCT TAT
6543
SER ARG SER ARG SER ILE GLU VAL ASN TYR VAL PRO PHE ASP GLU LEU LEU GLN ASN SER
AGT CGC AGC CGA AGT ATA GAG GTA AAC TAT GTA CCG TTT GAT GAG TTG CTG CAA AAT AGC
6603
ASP ILE VAL THR LEU HIS VAL PRO LEU ASN THR ASP THR HIS TYR ILE ILE SER HIS GLU
GAT ATC GTT ACG CTT CAT GTG CCG CTC AAT ACG GAT ACG CAC TAT ATT ATC AGC CAC GAA
6663
GLN ILE GLN ARG MET LYS GLN GLY ALA PHE LEU ILE ASN THR GLY ARG GLY PRO LEU VAL
CAA ATA CAG AGA ATG AAG CAA GGA GCA TTT CTT ATC AAT ACT GGG CGC GGT CCA CTT GTA

FIGURE 8 (11/23)

6723 ASP THR TYR GLU LEU VAL LYS ALA LEU GLY ASN GLY LYS LEU GLY GLY ALA ALA LEU ASP
GAT ACC TAT GAG TTT GGT AAA GCA TTA GAA AAC GGG AAA CTG GGC GGT GCC GCA TTG GAT

6783 VAL LEU GLU GLY GLU GLU PHE PHE TYR SER ASP CYS THR GLN LYS PRO ILE ASP ASN
GTA TTG GAA GGA GAG GAA GAG TTT TTC TAC TCT GAT TGC ACC CAA AAA CCA ATT GAT AAT

6843 GLN PHE LEU LEU LYS LEU GLN ARG MET PRO ASN VAL ILE ILE THR PRO HIS THR ALA TYR
CAA TTT TTA CTT AAA CTT CAA AGA ATG CCT AAC GTG ATA ATC ACA CCG CAT ACG GCC TAT

6903 TYR THR GLU GLN ALA LEU ARG ASP THR VAL GLU LYS THR ILE LYS ASN CYS LEU ASP PHE
TAT ACC GAG CAA GCG TTG CGT GAT ACC GTT GAA AAA ACC ATT AAA AAC TGT TTG GAT TTT

6963 ~~VADA METASN ARG ILE LYS VAL ALA ILE LEU PHE GLY GLY CYS SER~~
GAA AGG AGA CAG GAG CATGAAT AGA ATA AAA GTT GCA ATA CTG TTT GGG GGT TGC TCA
GLU ARG ARG GLN GLU HISGLU

7021 GLU GLU HIS ASP VAL SER VAL LYS SER ALA ILE GLU ILE ALA ALA ASN ILE ASN LYS GLU
GAG GAG CAT GAC GAT TCG GTA AAA TCT GCA ATA GAG ATA GCC GCT AAC ATT AAT AAA GAA

7081 LYS TYR GLU PRO LEU TYR ILE GLY ILE THR LYS SER GLY VAL TRP LYS MET CYS GLU LYS
AAA TAC GAG CCG TTA TAC ATT GGA ATT ACG AAA TCT GGT GTA TGG AAA ATG TGC GAA AAA

7141 PRO CYS ALA GLU TRP GLU ASN ASP ASN CYS TYR SER ALA VAL LEU SER PRO ASP LYS LYS
CCT TGC GCG GAA TGG GAA AAC GAC AAT TGC TAT TCA GCT GTA CTC TCG CCG GAT AAA AAA

7201 MET HIS GLY LEU LEU VAL LYS LYS ASN HIS GLU TYR GLU ILE ASN HIS VAL ASP VAL ALA
ATG CAC GGA TTA CTT GTT AAA AAG AAC CAT GAA TAT GAA ATC AAC CAT GTT GAT GTA GCA

7261

FIGURE 8 (12/23)

PHE SER ALA LEU HIS GLY LYS SER GLY GLU ASP GLY SER ILE GLN GLY LEU PHE GLU LEU
 TTT TCA GCT TTG CAT GGC AAG TCA TCA GGT GAA GAT GGA TCC ATA CAA GGT CTG TTT GAA TTG
 7321
 SER GLY ILE PRO PHE VAL GLY CYS ASP ILE GLN SER SER ALA ILE CYS MET ASP LYS SER
 TCC GGT ATC CCT TTT GTA GGC TGC GAT ATT CAA AGC TCA GCA ATT TGT ATG GAC AAA TCG
 7381
 LEU THR TYR ILE VAL ALA LYS ASN ALA GLY ILE ALA THR PRO ALA PHE TRP VAL ILE ASN
 TTG ACA TAC ATC GTT GCG AAA AAT GCT GCG ATA GCT ACT CCC GCC TTT TGG GTT ATT AAT
 7441
 LYS ASP ARG PRO VAL ALA ALA THR PHE THR TYR PRO VAL PHE VAL LYS PRO ALA ARG
 AAA GAT GAT AGG CCG GTG GCA GCT ACG TTT ACC TAT CCT GTT TTT GTT AAG CCG GCG CGT
 7501
 SER GLY SER SER PHE GLY VAL LYS LYS VAL ASN SER ALA ASP GLU LEU ASP TYR ALA ILE
 TCA GGC TCA TCC TTC GGT GTG AAA AAA GTG AAT AGC GCG GAC GAA TTG GAC TAC GCA ATT
 7561
 GLU SER ALA ARG GLN TYR ASP SER LYS ILE LEU ILE GLU GLN ALA VAL SER GLY CYS GLU
 GAA TCG GCA AGA CAA TAT GAC AGC AAA ATC TTA ATT GAG CAG GCT GTT TCG GGC TGT GAG
 7621
 VAL GLY CYS ALA VAL LEU GLY ASN SER ALA ALA LEU VAL GLY GLU VAL ASP GLN ILE
 GTC GGT TGT GCG GTA TTG GGA AAC AGT GCC GCG TTA GTT GGT GGC GAG GTG GAC CAA ATC
 7681
 ARG LEU GLN TYR GLY ILE PHE ARG ILE HIS GLN GLU VAL GLU PRO GLU LYS GLY SER GLU
 AGG CTG CAG TAC GGA ATC TTT CGT ATT CAT CAG GAA GTC GAG CCG GAA AAA GGC TCT GAA
 7741
 ASN ALA VAL ILE THR VAL PRO ALA ASP LEU SER ALA GLU GLU ARG GLY ARG ILE GLN GLU
 AAC GCA GTT ATA ACC GTT CCC GCA GAC CTT TCA GCA GAG GAG CGA GGA CGG ATA CAG GAA
 7801
 THR ALA LYS LYS ILE TYR LYS ALA LEU GLY CYS ARG GLY LEU ALA ARG VAL ASP MET PHE
 ACG GCA AAA AAA ATA TAT AAA GCG CTC GGC TGT AGA GGT CTA GCC CGT GTG GAT ATG TTT

7861 LEU GLN ASP ASN GLY ARG ILE VAL LEU ASN GLU VAL ASN THR LEU PRO GLY PHE THR SER
 TTA CAA GAT AAC GGC CGC ATT GTA CTG AAC GAA GTC AAT ACT CTG CCC GGT TTC ACG TCA
 7921 TYR SER ARG TYR PRO ARG MET MET ALA ALA GLY ILE ALA LEU PRO GLU LEU ILE ASP
 TAC AGT CGT TAT CCC CGT ATG ATG GCC GCT GCA GGT ATT GCA CTT CCC GAA CTG ATT GAC
 7981 ARG LEU ILE VAL LEU ALA LEU LYS GLY
 CGC TTG ATC GTA TTA GCG TTA AAG GGG TGATAAGC ATG GAA ATA GGA TTT ACT TTT TTA GAT
 VAX MET GLU ILE GLY PHE THR PHE LEU ASP
 8043 GLU ILE VAL HIS GLY VAL ARG TRP ASP ALA LYS TYR ALA THR TRP ASP ASN PHE THR GLY
 GAA ATA GTA CAC GGT GTT CGT TGG GAC GCT AAA TAT GCC ACT TGG GAT AAT TTC ACC GGA
 8103 LYS PRO VAL ASP GLY TYR GLU VAL ASN ARG ILE VAL GLY THR TYR GLU LEU ALA GLU SER
 AAA CCG GTT GAC GGT TAT GAA GTA AAT CGC ATT GTA GGG ACA TAC GAG TTG GCT GAA TCG
 8163 LEU LEU LYS ALA LYS GLU LEU ALA ALA THR GLN GLY TYR GLY LEU LEU TRP ASP GLY
 CTT TTG AAG GCA AAA GAA GAA CTG GCT GCT ACC CAA GGG TAC GGA TTG CTT CTA TGG GAC GGT
 8223 TYR ARG PRO LYS ARG ALA VAL ASN CYS PHE MET GLN TRP ALA ALA GLN PRO GLU ASN ASN
 TAC CGT CCT AAG CGT GCT GTA AAC TGT TTT ATG CAA TGG GCT GCA CAG CCG GAA AAT AAC
 8283 LEU THR LYS GLU SER TYR TYR PRO ASN ILE ASP ARG THR GLU MET ILE SER LYS GLY TYR
 CTG ACA AAG GAA AGT TAT TAT CCC AAT ATT GAC CGA ACT GAG ATG ATT TCA AAA GGA TAC
 8343 VAL ALA SER LYS SER SER HIS SER ARG GLY SER ALA ILE ASP LEU THR LEU TYR ARG LEU
 GTG GCT TCA AAA TCA AGC CAT AGC CGC GGC AGT GCC ATT GAT CTT ACG CTT TAT CGA TTA
 8403 ASP THR GLY GLU LEU VAL PRO MET GLY SER ARG PHE ASP PHE MET ASP GLU ARG SER HIS
 GAC ACG GGT GAG CTT GTA CCA ATG GGG AGC CGA TTT GAT TTT ATG GAT GAA CGC TCT CAT

FIGURE 8 (14/23)

8463 HIS ALA ALA ASN GLY ILE SER CYS ASN GLU ALA GLN ASN ARG ARG ARG LEU ARG SER ILE
CAT GCG GCA AAT GGA ATA TCA TGC AAT GAA GCG CAA AAT CGC AGA CGT TTG CGC TCC ATC
8523 MET GLU ASN SER GLY PHE GLU ALA TYR SER LEU GLU TRP TRP HIS TYR VAL LEU ARG ASP
ATG GAA AAC AGT GGG TTT GAA GCA TAT AGC CTC GAA TGG TGG CAC TAT GTA TTA AGA GAC
8583 GLU PRO TYR PRO ASN SER TYR PHE ASP PHE PRO VAL LYS
GAA CCA TAC CCC AAT AGC TAT TTT GAT TTC CCC GTT AAA TAAA CTT TTA ACC GTT GCA
8641 CCG ACA AAC TAT ATA AGC TAA CTC TTT CCG CAG GAA ACC CGA CGT ATG TAA CTG GTT CTT
8701 AGG GAA TTT ATA TAT AGT AGA TAG TAT TGA AGA TGT AAG GCA GAG CGA TAT TGC GGT CAT
8761 TAT CTG CGT GCG CTG CAA GAT AGC CTG ATA ATA AGA CTG ATC GCA TAG AGG GGT GGT
8821 ATT TCA CAC CGC CCA TTG TCA ACA GGC AGT TCA GCC TCG TTA AAT TCA GCA TGG GTA TCA
8881 CTT ATG AAA ATT CAT CTA CAT TGG TGA TAA TAG TAA ATC CAG TAG GGC GAA ATA ATT GAC
8941 TGT AAT TTA CCG GGC AAA ACG GCA CAA TCT CAA ACG AGA TTG TGC CGT TTA AGG GGA AGA
9001
TTC TAG AAA TAT TTC ATA CTT CCA ACT ATA TAG TTA AGG AGG AGA CTG AAA ATG AAG AAG
9061 LEU PHE PHE LEU LEU LEU LEU PHE LEU ILE TYR LEU GLY TYR ASP TYR VAL ASN GLU
TTG TTT TTT TTA TTG TTA TTC TTA ATA TAC TTA GGT TAT GAC TAC GTT AAT GAA

Vary

MET LYS LYS

FIGURE 8 (15/23)

9121
 ALA LEU PHE SER GLN GLU LYS VAL GLU PHE GLN ASN TYR ASP GLN ASN PRO LYS GLU HIS
 GCA CTG TTT TCT CAG GAA AAA GTC GAA TTT CAA AAT TAT GAT CAA AAT CCC AAA GAA CAT.
 9181
 LEU GLU ASN SER GLY THR SER GLU ASN THR GLN GLU LYS THR ILE THR GLU GLN VAL
 TTA GAA AAT AGT GGG ACT TCT GAA AAT ACC CAA GAG AAA ACA ATT ACA GAA CAG GTT
 9241
 TYR GLN GLY ASN LEU LEU ILE ASN SER LYS TYR PRO VAL ARG GLN GLU SER VAL LYS
 ATAT CAA GGA AAT CTG CTA TTA ATC AAT AGT AAA TAT CCT GTT CGC CAA GAA AGT GTG AAG
 9301
 SER ASP ILE VAL ASN LEU SER LYS HIS ASP GLU LEU ILE ASN GLY TYR GLY LEU LEU ASP
 TCAT GAT ATC GTG AAT TTA TCT AAA CAT GAC GAA TTA ATA AAT GGA TAC GGC TTG CTT GAT
 9361
 ASN ILE TYR MET SER LYS GLU ILE ALA GLN LYS PHE SER GLU MET VAL ASN ASP ALA
 AGT AAT ATT TAT ATG TCA AAA GAA ATA GCA CAA AAA TTT TCA GAG ATG GTC AAT GAT GCT
 9421
 VAL LYS GLY GLY VAL SER HIS PHE ILE ILE ASN SER GLY TYR ARG ASP PHE ASP GLU GLN
 GTA AAG GGT GGC GTT AGT CAT TTT ATT ATT AAT AGT GGC TAT CGA GAC TTT GAT GAG CAA
 9481
 SSER VAL LEU TYR GLN GLU MET GLY ALA GLU TYR ALA LEU PRO ALA GLY TYR SER GLU HIS
 AGT GTG CTT TAC CAA GAA ATG GGG GCT GAG TAT GCC TTA CCA GCA GCA TAT AGT GAG CAT
 9541
 ASN SER GLY LEU SER LEU ASP VAL GLY SER SER LEU THR LYS MET GLU ARG ALA PRO GLU
 AAT TCA GGT TTA TCA CTA GAT GTA GGA TCA AGC TTG ACG AAA ATG GAA CGA GCC CCT GAA
 9601
 TRP ILE GLU GLU ASN ALA TRP LYS TYR GLY PHE ILE LEU ARG TYR PRO GLU ASP
 GGA AAG TGG ATA GAA GAA AAT GCT TGG AAA TAC GGG TTC ATT TTA CGT TAT CCA GAG GAC
 9661
 LYS THR GLU LEU THR GLY ILE GLN TYR GLU PRO TRP HIS ILE ARG TYR VAL GLY LEU PRO
 AAA ACA GAG TTA ACA GGA ATT CAA TAT GAA CCA TGG CAT ATT CGC TAT GTT TTA CCA
 9721

9781	HIS SER ALA ILE MET LYS GLU LYS ASN PHE VAL LEU LEU GLU TYR MET ASP TYR LEU LYS	9781	AAA CTA AAA
	CAT AGT GCG ATT ATG AAA GAA AAG AAT TTC GTT CTC GAG GAA TAT ATG GAT TAC CTA AAA		
9841	GLU LYS THR ILE SER VAL SER VAL ASN GLY GLU LYS TYR GLU ILE PHE TYR TYR PRO	9841	AAA CCT
	GAA AAA ACC ATT TCT GTT GAT AAT GGG GAA AAA TAT GAG ATC TTT TAT TAT CCT		
9901	THR LYS ASN THR THR ILE HIS VAL PRO THR ASN LEU ARG TYR GLU ILE SER GLY ASN	9901	AAA AAC
	AAT ACC ACC ATT CAT GTG CCG ACT AAT AAT CTT CGT TAT GAG ATA TCA GGA AAC		
9961	ILE ASP GLY VAL ILE VAL THR VAL PHE PRO GLY SER THR HIS THR ASN SER ARG ARG	9961	AGG
	AAT ATA GAC GGT GTA ATT GTG ACA GTG TTT CCC GGA TCA ACA CAT ACT AAT TCA AGG AGG		
10021	TAA GGA TGG CGG AAT GAA ACC AAC GAA ATT AAT GAA CAG CAT TAT TGT ACT AGC ACT TTT	10021	ATG
	GGA GTA ACG TTA GCT TTT TAA TTT AAA ACC CAC GTT AAC TAG GAC ATT GCT ATA CTA ATG		
10081	ATA CAA CTT AAA CAA AAG AATTAGAGG AAA TTA TA TTG GGA AAA ATA TTA TCT AGA GGA TTG	10081	LEU
10143	LEU ALA LEU TYR LEU VAL THR LEU ILE TRP LEU VAL LEU PHE LYS LEU GLN TYR ASN ILE	10143	ATT
	CTA GCT TTA TAT TTA GTG ACA CTA ATC TGG TTA GTG TTA TTC AAA TTA CAA TAC AAT ATT		
10203	LEU SER VAL PHE ASN TYR HIS GLN ARG SER LEU ASN LEU THR PRO PHE THR ALA THR GLY	10203	GGG
	TTA TCA GTA TTT AAT TAT CAT CAA AGA AGT CTT AAC TTG ACT CCA TTT ACT GCT ACT GGG		
10263	ASN PHE ARG GLU MET ILE ASP ASN VAL ILE ILE PHE ILE PRO PHE GLY LEU LEU ASN	10263	AAT
	AAT TTC AGA GAG ATG ATA GAT AAT GTT ATA ATC TTT ATT CCA TTT GGC TTG CTT TTG AAT		

FIGURE 8(17/23)

10323 VAL ASN PHE LYS GLU ILE GLY PHE LEU PRO LYS PHE ALA PHE VAL LEU VAL LEU SER LEU
 GTC AAT TTT AAA GAA ATC GGA TTT TTA CCT AAG TTT GCT TTT GTA CTG GTT TTA AGT CTT
 10383 THR PHE GLU ILE ILE GLN PHE ILE PHE ALA ILE GLY ALA THR ASP ILE THR ASP VAL ILE
 ACT TTT GAA ATA ATT CAA TTT ATC TTC GCT ATT GGA GGG ACA GAC ATA ACA GAT GTA ATT
 10443 THR ASN THR VAL GLY GLY PHE LEU GLY LEU LYS LEU TYR GLY LEU SER ASN LYS HIS MET
 ACA AAT ACT GTT GGA GGC TTT CTT GGA CTG AAA TTA TAT GGT TTA AGC AAT AAG CAT ATG
 10503 ASN GLN LYS LYS LEU ASP ARG VAL ILE ILE PHE VAL GLY ILE LEU LEU VAL LEU LEU
 AAT CAA AAA AAA TTA GAC AGA GTT ATT ATT TTT GTA GGT ATA CTT TTG CTC GTA TTA TTG
 10563 LEU VAL TYR ARG THR HXS LEU ARG ILE ASN TYR VAL
 CTC GTT TAC CGT ACC CAT TTA AGA ATA AAT TAC GTG TAAG ATG TCT AAA TCA AGC AAT
 10621 CTG ATC TTT CAT ACA CAT AAA GAT ATT GAA TGA ATT GGA TTA GAT GGA AAA CGG GAT GTG
 10681 GGG AAA CTC GCC CGT AGG TGT GAA GTG AGG GGA AAA CCG GTG ATA AAG TAA AAA GCT TAC
 10741 CTA ACA CTA TAG TAA CAA AGA AAG CCC AAT TAT CAA TTT TAG TGC TGA GGA ATT GGT CTC
 10801 TTT AAT AAA TTT CCT TAA CGT TGT AAA TCC GCA TTT TCC TGA CGG TAC CCC

Ib brin(-)

1 CAA AAT ATC ACC TCA TTT TTG AGA CAA GTC TTA TGA GAC GCT CTT AAC TAT GAT TTT ATC
61 AGT CTA CTA CAT TTG TAT CAA TAG AGT ACA CTC TAT TGA TAT ATA ATT GAA CTA ATA AAT

121 **Transposase** MET LYS ILE ALA ARG GLY ARG GLU LEU LEU THR
TGA AAA TAC AGA AAT GGA ATGATACTG AA ATG AAA ATT GCG AGA GGT AGA GAA TTG CTT ACA
182 PRO GLN GLN ARG GLN ALA PHE MET GLN ILE PRO GLU ASP GLU TRP ILE LEU GLY THR TYR
CCG GAA CAG AGA CAG GCT TTT ATG CAA ATC CCT GAA GAT GAA TGG ATA CTG GGG ACC TAC
242 PHE THR PHE SER LYS ARG ASP LEU GLU ILE VAL ASN LYS ARG ARG GLU GLU ASN ARG
TTC ACT TTT TCC AAA CCG GAT TTA GAA ATA GTT AAT AAG CGA AGG AGG GAA GAA AAC CGT
302 LEU GLY PHE ALA VAL GLN LEU ALA VAL LEU ARG TYR PRO GLY TRP PRO TYR THR HIS ILE
TTA GGA TTT GCT GTT CAA TTA GCT GTT CTT CGG TAT CCC GGT TGG CCA TAC ACT CAT ATC
362 LYS SER ILE PRO ASP SER VAL ILE GLN TYR ILE SER LYS GLN ILE GLY VAL SER PRO SER
AAA AGC ATC CCA GAT TCG GTC ATA CAA TAT ATA TCG AAA CAG ATT GGT GTT AGT CCA TCC
422 SER LEU ASP HIS TYR PRO GLN ARG GLU ASN THR LEU TRP ASP HIS LEU LYS GLU ILE ARG
TCG CTT GAT CAT TAT CCT CAA AGG GAA AAT ACA CTT TGG GAT CAT TTG AAA GAA ATT CGA

FIGURE 8 (19/23)

482 SER GLU TYR ASP PHE VAL THR PHE THR LEU SER GLU TYR ARG MET THR PHE LYS TYR LEU
 AGT GAA TAC GAC TTT GTA ACT TTT ACC CTG AGT GAA TAT CGA ATG ACA TTT AAG TAC CTT

542 HIS GLN LEU ALA LEU GLU ASN GLY ASP ALA ILE HIS LEU LEU HIS GLU CYS ILE ASP PHE
 CAT CAA TTA GCT TTG GAA AAT GGT GAT GCC ATT CAT CTA CTG CAT GAA TGC ATA GAT TTT

602 LEU ARG LYS ASN LYS ILE LEU PRO ALA ILE THR THR LEU GLU ARG MET VAL TRP GLU
 CTA AGA AAA AAC AAA ATT ATA CTG CCT GCT ATC ATC ACT ACA CTT GAA AGA ATG GTG TGG GAA

662 ALA ARG ALA MET ALA GLU LYS LYS LEU PHE ASN THR VAL SER LYS SER LEU THR ASN GLU
 GCA AGG GCA ATG GCT GAA AAG AAG CTA TTT AAT ACG GTT AGT AAA TCT CTA ACA AAT GAG

722 GLN LYS GLU LYS LEU GLU GLY ILE ILE THR SER GLN HIS PRO SER GLU SER ASN LYS THR
 CAA AAA GAA AAG CTT GAA GGG ATT ATT ACC TCG CAG CAT CCA TCC GAA TCC AAT AAA ACG

782 ILE LEU GLY TRP LEU LYS GLU PRO PRO GLY HIS PRO SER PRO GLU THR PHE LEU LYS ILE
 ATA TTG GGT TGG TTA AAA GAG CCA CCG GGT CAT CCT TCA CCC GAA ACT TTT CTA AAA ATA

842 ILE GLU ARG LEU GLU TYR ILE ARG GLY MET ASP LEU GLU THR VAL GLN ILE SER HIS LEU
 ATA GAA CGA CTC GAA TAC ATA CGA GGA ATG GAT TTA GAA ACA GTG CAA ATT AGT CAT TTG

902 HIS ARG ASN ARG LEU LEU GLN LEU SER ARG LEU GLY SER ARG TYR GLU PRO TYR ALA PHE
 CAC CGT AAC CGC CTG TTG CAG CTG TCT CGC TTA GGC TCA AGA TAC GAG CCG TAT GCA TTC

962 ARG ASP PHE GLN GLU ASN LYS ARG TYR SER ILE LEU THR ILE TYR LEU LEU GLN LEU THR
 CGT GAC TTT CAA GAA AAT AAA CGT TAT TCG ATA TTA ACC ATC TAT TTA TTA CAA CTT ACT

1022 GLN GLU LEU THR ASP LYS ALA PHE GLU ILE HIS ASP ARG GLN ILE LEU SER LEU LEU SER
 CAG GAG CTA ACG GAT AAA GCG TTT GAA ATT CAT GAT AGG CAA ATA CTT AGT TTG TTA TCA

1082 LYS GLY ARG LYS ALA GLN GLU GLU ILE GLN LYS LYS GLN ASN GLY LYS LEU ASN GLU LYS
AAA GGT CGT AAG GCT CAA GAG GAA ATC CAG AAA CAA AAC GGT AAA AAG CTA AAT GAG AAA
1142 VAL ILE HIS PHE THR ASN ILE GLY GLN ALA LEU ILE LYS ALA ARG GLU GLU LYS LEU ASP
GTT ATA CAC TTT ACG AAC ATC GGA CAA GCA TTA ATT AAA GCA AGA GAG GAA AAA TTA GAC
1202 VAL PHE LYS VAL LEU GLU SER VAL ILE GLU TRP ASN THR PHE VAL SER SER VAL GLU GLU
GTT TTT AAG GTT TTA GAA TCG GTT ATT GAA TGG AAT ACC TTT GTC TCT TCA GTA GAA GAG
1262 ALA GLN GLU LEU ALA ARG PRO ALA ASP TYR ASP TYR LEU ASP LEU LEU GLN LYS ARG PHE
GCT CAG GAA CTT GCA CGT CCT GCC GAC TAT GAT TAT TTA GAC TTA CTG CAA AAA CGG TTT
1322 TYR SER LEU ARG LYS TYR THR PRO THR LEU LEU ARG VAL LEU GLU PHE HIS SER THR LYS
TAT TCA CTA AGA AAA TAT ACG CCA ACG CTA TTA AGA GTA TTG GAA TTT CAT TCT ACA AAG
1382 ALA ASN GLU PRO LEU LEU GLN ALA VAL GLU ILE ILE ARG GLY MET ASN GLU SER GLY LYS
GCA AAT GAG CCA CTT TTA CAA GCT GTT GAG ATT ATC CGA GGA ATG AAC GAA TCT GGA AAG
1442 ARG LYS VAL PRO ASP ASP SER PRO VAL ASP PHE ILE SER LYS ARG TRP LYS ARG HIS LEU
CGA AAA GTG CCT GAT GAT GAC TCA CCT GTG GAT TTT ATT TCA AAA CGA TGG AAA AGA CAT TTA
1502 TYR GLU ASP ASP GLY THR THR ILE ASN ARG HIS TYR TYR GLU MET ALA VAL LEU THR GLU
TAC GAG GAT GAT GGT ACA ACA ATT AAT AAT CGT CAT TAC TAT GAA ATG GCT GTT TTA ACA GAA
1562 LEU ARG GLU HIS VAL ARG ALA GLY ASP VAL SER ILE VAL GLY SER ARG GLN TYR ARG ASP
CTT CGG GAG CAT GTT CGG GCA GGA GAT GTT TCC ATT GTT GGC AGC AGA CAA TAT AGG GAT

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FIGURE 8 (21/23)

1622 PHE GLU GLU TYR LEU PHE SER GLU ASP THR TRP ASN GLN SER LYS GLY ASN THR ARG LEU
 TTT GAG GAA TAT TTG TTT TCG GAA GAT ACA TGG AAT CAA TCG AAG GGG AAT ACG AGA TTA
 1682 SER VAL SER LEU SER PHE GLU ASP TYR ILE THR GLU ARG THR SER SER PHE ASN GLU ARG
 TCA GTT AGT TTA TCA TTC GAA GAT TAT ATA ACG GAG AGA ACC AGC AGC TTT AAT GAA AGG
 1742 LEU LYS TRP LEU ALA ALA ASN SER ASN LYS LEU ASP GLY VAL SER LEU GLU LYS GLY LYS
 TTA AAG TGG TTA GCT GCC AAT TCC AAT AAG TTA GAT GGG GTT TCT CTT GAA AAA GGA AAG
 1802 LEU SER LEU ALA ARG LEU GLU LYS ASP VAL PRO GLU GLU ALA LYS LYS PHE SER ALA SER
 CTA TCA CTT GCA CGC TTA GAA AAA GAT GTT CCA GAA GAA GCA AAA AAA TTT AGT GCA AGC
 1862 LEU TYR GLN MET LEU PRO ARG ILE LYS LEU THR ASP LEU LEU MET ASP VAL ALA HIS ILE
 CTT TAT CAG ATG CTA CCA AGA ATA AAA TTA ACT GAT TTA CTC ATG GAT GTG GCC CAT ATA
 1922 THR GLY PHE HIS GLU GLN PHE THR HIS ALA SER ASN ASN ARG LYS PRO ASP LYS GLU GLU
 ACA GGA TTT CAT GAG CAA TTC ACT CAT GCT TCC AAT AAT CGA AAA CCA GAT AAG GAA GAA
 1982 THR ILE ILE ILE MET ALA ALA LEU LEU GLY MET GLY MET ASN ILE GLY LEU SER LYS MET
 ACA ATC ATT ATC ATG GCT GCT GCC CTT TTA GGA ATG GGA ATG AAT ATT GGC TTG AGC AAG ATG
 2042 ALA GLU ALA THR PRO GLY LEU THR TYR LYS GLN LEU ALA ASN VAL SER GLN TRP ARG MET
 GCC GAA GCC ACA CCC GGA CTT ACA TAT AAG CAA CTA GCC AAT GTA TCT CAA TGG CGC ATG
 2102 TYR GLU ASP ALA MET ASN LYS ALA GLN ALA ILE LEU VAL ASN PHE HIS HIS LYS LEU GLN
 TAT GAA GAT GCC ATG AAT AAA GCC CAA GCC ATA TTA GTA AAC TTT CAT CAT AAA TTA CAA
 2162 LEU PRO PHE TYR TRP GLY ASP GLY THR THR SER SER ASP GLY MET ARG MET GLN LEU
 TTG CCT TTC TAT TGG GGC GAC GGT ACA ACA TCT TCG TCA GAT GGT ATG AGA ATG CAG CTA

2222 GLY VAL SER SER LEU HIS ALA ASP ALA ASN PRO HIS TYR GLY THR GLY LYS GLY ALA THR
 GGT GTT TCA TCA CTA CAT GCA GAT GCA AAT CCA CAT TAT GGA ACT GGA AAA GGA GCC ACC
 2282 ILE TYR ARG PHE THR SER ASP GLN PHE SER SER TYR TYR THR LYS ILE ILE HIS THR ASN
 ATC TAC CGA TTT ACA AGT GAT CAA TTC TCT TCT TAC TAC ACA AAG ATT ATT CAT ACT AAT
 2342 SER ARG ASP ALA ILE HIS VAL LEU ASP GLY LEU LEU HIS HIS GLU THR ASP LEU ASN ILE
 TCA AGA GAT GCG ATT CAT GTT TTG GAT GGT TTG TTA CAT CAT GAG ACG GAT CTA AAC ATA
 2402 GLU GLU HIS TYR THR ASP THR ALA GLY TYR THR ASP GLN ILE PHE GLY LEU THR HIS LEU
 GAG GAA CAT TAT ACA GAC ACT GCC GGT TAC ACT GAC CAA ATA TTC GGA CTG ACT CAT TTA
 2462 LEU GLY PHE LYS PHE ALA PRO ARG ILE ARG ASP LEU SER ASP SER LYS LEU PHE THR ILE
 TTA GGA TTT AAA TTT GCC CCA AGA ATA AGG GAT TTA TCG GAC TCA AAA TTA TTT ACG ATA
 2522 ASP LYS ALA SER GLU TYR PRO LYS LEU GLU ALA ILE LEU ARG GLY GLN ILE ASN THR LYS
 GAT AAA GCA AGT GAG TAT CCA AAA CTA GAA GCC ATT TTA CGT GGA CAA ATA AAT ACA AAG
 2582 VAL ILE LYS GLU ASN TYR GLU ASP VAL LEU ARG LEU ALA HIS SER ILE ARG GLU GLY THR
 GTC ATT AAA GAA AAT TAT GAG GAT GTT TTG CGA TTA GCT CAT TCT ATA AGG GAG GGA ACA
 2642 AGT TTC AGC ATC CCT TAT TAT GGG GAA GCT AGG TTC CTA TTC AAG ACA AAA CAG CTT AGC
 VAL SER ALA SER LEU ILE MET GLY LYS LEU GLY SER TYR SER ARG GLN ASN SER LEU ALA
 GTT TCA GCA TCC CTT ATT ATG GGG AAG CTA GGT TCC TAT TCA AGA CAA AAC AGC TTA GCT
 2702 THR ALA LEU ARG GLU MET GLY ARG ILE GLU LYS THR ILE PHE ILE LEU ASN TYR ILE SER
 ACA GCC TTA CGT GAG ATG GGC CGA ATA GAA AAA ACG ATC TTT ATT TTG AAT TAT ATA TCG

FIGURE 8 (23/23)

2762 ASP GLU SER LEU ARG ARG LYS ILE GLN ARG GLY LEU ASN LYS GLY GLU ALA MET ASN GLY
 GAT GAA TCA TTA AGA AGA AAA ATA CAA AGA GGA TTTG AAT AAA GGA GAA GCC ATG AAT GGA
 2822 LEU ALA ARG ALA ILE PHE PHE GLY LYS GLN GLY LEU ARG GLU ARG THR ILE GLN HIS
 TTG GCA AGA GCT ATT TTC TTC GGA AAA CAA GGT GAG CTT AGA GAA CGC ACC ATA CAG CAT
 2882 GLN LEU GLN ARG ALA SER ALA LEU ASN ILE ILE ILE SER ILE TRP ASN THR
 CAA TTG CAA AGA GCC AGT GCT TTA AAC ATA ATT ATC AAT GCT ATA AGT ATT TGG AAT ACT
 2942 TCT CCA CCT AAC AAC AGC AGT TGA ATA TAA AAA ACG GAC AGG TAG CTT TAA TGA AGA TTT
 LEU HIS LEU THR THR ALA VAL GLU TYR LYS LYS ARG THR GLY SER PHE ASN GLU ASP LEU
 CTC CAC CTA ACA ACA GCA GGT GAA TAT AAA AAA CGG ACA GGT AGC TTT AAT GAA GAT TTG
 3002 LEU HIS HIS MET SER PRO LEU GLY TRP GLU HIS ILE ASN LEU LEU GLY GLU TYR HIS PHE
 TTA CAC CAT ATG TCG CCC TTA GGT TGG GAA CAT ATT AAT TTA CTA GGA GAA TAC CAT TTT
 3062 ASN SER GLU LYS VAL VAL SER LEU ASN SER LEU ARG PRO LEU LYS LEU SER
 AAC TCA GAG AAA GTA GTC TCA TTA AAT TCT TTA AGA CCA CTA AAA CTT TCT TAA CGT TG
 3121 TTA AAA ACG AGG GAT TCG TCA GGA AAA TAG GCT TAG CGT TGT AAA TCC GCA TTT TCC TGA
 3181 CGC TAC CCC

SacI

GAGCTCTTCCTTCAACGCACTTCTGTACCAAGAGTTGTTGTC	42
CATTGATCACTAACATAGCTTCCCCCTGCTTTCTTCAAGCCCTTTGTGCATAAAATCGTTAGATTTTCA	111
TCATAAAATACGAGAAAGACACAGGAAGACCGCAAAATTTTCTTTTCTTAGGTACACTGAATG	180
TAACCTTAAAGAAAAAGGAAGGAAATGATGAAAAAATGCGGTTTATTGGAGGG	244
N S P E Y S V S L T S A A S V I Q A I D	304
AATTCTCCAGAACTACTCAGTGTCACTAACCTCAGCAGCAAGTGTGATCCAAAGCTATTGAC	364
P L K Y E V M T I G I A P T M D W Y W Y	424
CCGCTGAAATATGAAGTAATGACCATTTGGCATCGCACCAACAATGGATTGGTATTGGTAT	484
Q G N L A N V R N D T W L E D H K N C H	544
CAAGGAAACCTCGCGAATGTTGCAATGATGATCTTGGCTAGAAAGATCACAACAACTGTGAC	604
Q L T F S S Q G F I L G E K R I V P D V	664
CAGCTGACTTTTCTAGCCAAAGGATTTATATATTAGGAGAAAAACGAATCGTCCCTGATGTC	724
L F P V L H G K Y G E D G C I Q G L L E	
CTCTTTCCAGTCTTGCAATGGGAAGTATGGCGAGGATGGCTGTATCCAAAGGACTGCTTGAA	
L M N L P Y V G C H V A A S A L C M N K	
CTAATGAACCTGCCCTTATGTTGGTTGCCATGTGCTGCTCCCTCCGCTATGATGAACAAA	
W L L H Q L A D T M G I A S A P T L L L	
TGGCTCTTGCACTCAACTTGCTGTATACCATGGGAATCGCTAGTGTCTCCACTTTGCTTTTA	
S R Y E N D P A T I D R F I Q D H G F P	
TCCCCGCTATGAAAAACGATCCCTGCCACAATCGATCGTTTATTATCAAGACCATGGATTCCCG	

FIGURE 9(1/2)

I F I K P N E A G S B K G I T K V T D K	
ATCTTTATCAAGCCGAATGAAGCCGGTTCTTCAAAAGGGATCACAAGTAGTACTGACAAA	784
T A L Q S A L T T A F A Y G S T V L I Q	
ACAGCGCTCCAACTGTCATTAAAGCACTGCTTTTGGCTTACGGTTCTACTGTGTGATCCAA	844
K A I A G I E I G C G I L G N E Q L T I	
AAGCGGATAGCGGGTATTGAAAATTGGCTCGCGCATCTTAGGAAATGAGCAATTGACCGATT	904
G A C D A I S L V D G F F D F E E K Y Q	
GGTGCTTGATCGGATTTCTCTTGTGCGACGGTTTTTTTGTGATTTTGAAGAGAAATACCAA	964
L I S A T I T V P A P L P L A L E S Q I	
TTAATCAGCGCCACGATCACTGTCCAGCACCATTTGCCCTCTCGCGCTTGAAATCACAGATC	1024
K E Q A Q L L Y R N L G L T G L A R I D	
AAGGAGCAGGCACAGCTGCTTTATTCGAAAACCTTGGGATTGACGGGTCTGGCTCGAATCGAT	1084
F F V T N Q G A I Y L N E I N T M P G F	
TTTTTCGTACCAATCAAGGAGCGGATTTATTTAAACGAAATCAACACCATGCCCGGATTT	1144
T G H S R Y P A M M A E V G L S Y E I L	
ACTGGGCACTCCCGCTACCCAGCTATGATGGCGGAAGTCGGGTATCTCTACGAAATATTA	1204
V E Q L E A L A E E D K R *	
GTAGAGCAATTGCTGCACTGGCAGAGGAGGACAAACCGATGAACACATTACAATTGATCAATA	1267
AAAACCATCCATTGAAAAAATCAAGAGCCCCCGCACTTAGTGCTAGCTCCTTTTAGCGATCACGATG	1336
TTTACCTGCAG	1347
PstI	

FIGURE 9 (2/2)

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VaaC  --HKKIAVLFGGNSPEYSVSLTSAASVIOAIDPLKYEVMTIGIAPTHDMYNYQGNLANVRNDTWLEDHKNCHQLTFSSQGFI LGEKRIVP-----D
VaaA  MNRIKVAILFGGCSEEHDSVKSATIEAANINKEKYEPLYIGITKSGVMKMCCKPCAENE  NDNCYSAVLS  PDKMMHGLLV  KKNHEYEINH  -----VD
Dd1A  MEKLRVGIVFGCKSAEHEVSLQSAKNIVDAIDKSRFDVVL  LGIDKGCQMH  VSDASNYLLN  ADDPAHIALR  PSATSLAQVP  GKHEHQLIDA  QNGQPLPTVD
Dd1B  -MTDKIAVLLGCTSAEREVS  LNSGAAVLAG  LREGGIDAYP  VDPKEVDVTQ  LKSHGFQKV-----

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~~<--1-->
 VLFPLVHGKY GEDGCIQGLL ELMNLPYVGC HVAASALCHN KWLHLQADT MGIASAPTLT LSRYEND-- PATIDRFIQD HGFPIFIKPN EAGSSKGIK
 VAFSALHGKS GEDGSIQGLF ELSGIPFVGC DIQSSAICHM KSLTYIVAKN AGIATPAFWV INKODRP--- -----VAAT FTYPVFVKPA RSGSSFVGVK
 VIFPIVHGTL GEDGSLOGHL RVANLPFVGS DVLASAACHM KDVTKRLLRD AGINIAPFIT LTRANRHNIS FAE---VESK LGLPLFVKPA NQGSVVGVSK
 --FIALHGRG GEDGTLOGHL ELMGLPYTGS GVNASALSMD KLRSKLLWQG AGLPVAPWVA LTRAEFEKGL SDKQLAEISA LGLPVIKPS REGSSVGMKS
 I CII IIIICCIICC CI IC C II CI I C IC CCC domain 2 ICCCII III IC I~~

VTDKTAALQSA LTTAFAYGST VLIQKAIAIGI EIGCGILGNE -QLTIGACDA ISLVGFFDF EEKYQLIS-- --ATITVPAP LPLALESQIK EQAQLLYRNL
VNSADELDYA IESARQYDSK ILIEQAVSGG EVGCAVLGNS AALVUGEVDQ IRLQYGIFRI HOEVEPEKGS ENAVITVPAD LSAERGRIQ ETAKKIYKAL
VTSEEQYATA VALAFEFDHK VIVEQGIKGR EIECAVLGND NP-----QAST CGEIVLTSDF YAYDTKYIDE DGAKWVVPAA IAPENDKIR AIAVQAYQTL
VVAENALQDA LRLAFQHDDEE VLIEKWLSP EFTVALIGEE IL-----P SIRIQPSGTF YDYEAKEYLSD ETQYFC-PAG LEASQEANLQ ALVLKAWTTL

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Vanc GLTGLARIDF FVTNQGA IYL NEINTMPGFT GHSRYPAMMA EVGLSYEILV EQIALAEED KR
VanA GCGRLARVDM FLQDNGRIVL NEVNTLPGET SYSRYPRMMA AAGIALPELI DRLIVLALKG
DdIA GCAGMARVDV FLTPENEVVI NEINTLPGET NISHYPKLWQ ASGLGYTDLI TRULIELALER HAANNALKTT H
DdIB GKKGWGRIDV MLDSDGQFYL LEANTSPGNT SHSLVPMAAR QAGMSFSQLV VRILELAD

I I C I C I C C C C I J J I I C I I I C I C C I I
domain 4

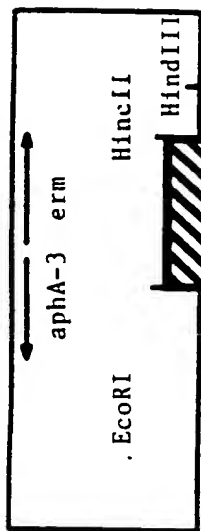
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FIGURE 10

FIGURE 11

FIGURE 12

A



B



C

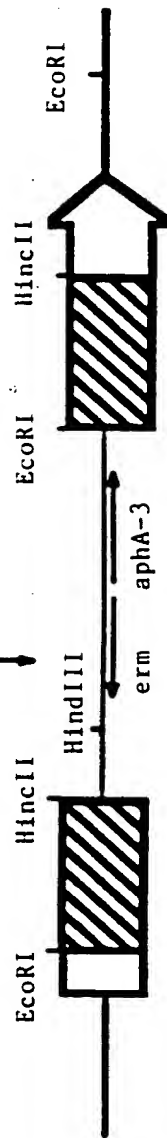
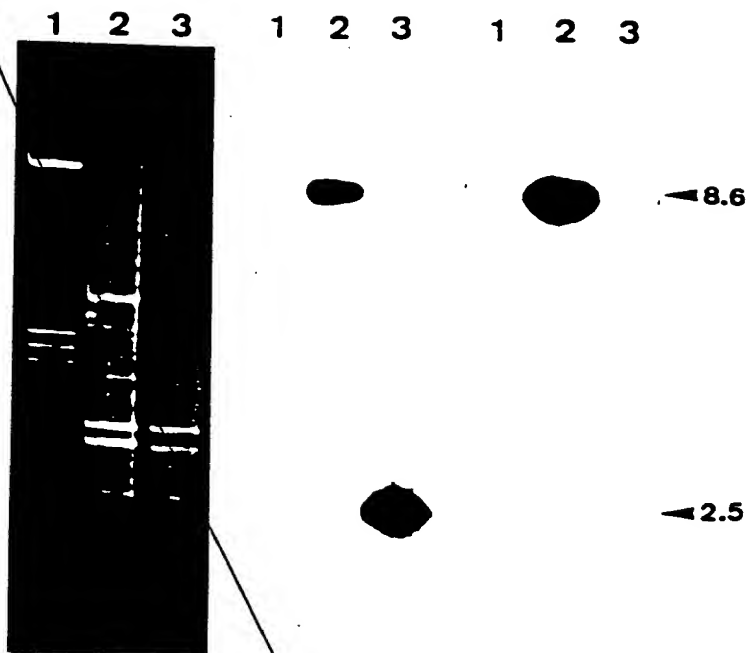


FIGURE 13



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FIGURE 14

VanR	--MSDKIL--	--IVDDHEHEIA--	DLVELYLKKNENYTVFK--YYTAK	AL	ECIDKSEI	DLAI	LDIML	56										
OmpR	MQENYKIL--	--VDDDDMRRLRA--	LLERYLTEQGFQVRS--VANAEQMDRL	LTRESF	HLML	LDLML	58											
PhoB	--MARRIL--	--VDEEAPIREMVCFL	EQNGFQPV	EAEDYDSAVNQ	LN	EPWDL	ILLDWML	56										
Chey	--MADKELKFL	VVDDFSTMRRIVRNLLKELGFNNVEE	AE	AGVDALNK	LQA	GGFI	ISDWNM	60										
VanR	PGTSGLTICQK	IRDKHTY--	PIIMLTGKDTEVDKI	TGLTIGADDYIT	KPFRP	LEL	IARVKA	115										
OmpR	PGEDGLSICRR	LRSQSNPM--	PIIMVTAKGEEVDRI	VGLEIGADDYIP	KPFN	PREL	LARIKA	118										
PhoB	PGGSGIQFIKH	LKRESMTRDI	PPVMLTARGEEEDRV	GL	ETGADDYIT	KPFS	PKELVARIKA	118										
Chey	PINMDGLELLKT	IRADSAMSALEP	VLMTAEAKKENI	IAAAQAGASGY	VVKPF	TAA	TL EEKLNK	122										
VanR	QLRRYKK-FSG	VKEQNE	NI	VHSGLVIN	VNTH	ECYLN	EKQLSLTPTEFS	ILRI	CENKGN	V	176							
OmpR	VLRQANELPG	APSQEEA	VI	AFGKFKLN	LGTR	EMFREDE	PPML	TS	GFEF	AVL	KALVSHPREPL	180						
PhoB	VMRRI	SP----	MAVE	IE	MOGL	SLDPTSH	RV	MAGEE	PL	EMGP	TEFKLL	HHFFMT	HPER	VY	174			
Chey	IFEKLG	M	129															
VanR	SSEL	LFHEI	WG	DE	YFSKSNN	TI	TVH	IRHLR	EKMND	TIDN	PKYIK	TVWG	VGYK	IEK	231			
OmpR	SRDK	LMN	LARG	RE	YSAMER	-SIDV	QIS	RLRM	VE	EDPA	HP	RYIQ	TVWG	LG	YVFV	PDGSKA	239	
PhoB	SREQ	LLNH	VW	GT	NVYVEDR	-TVD	VH	IRRLR	-KAL	EP	GGH	DRM	VQ	TV	RG	TGYRE	STRE	229

FIGURE 15